Statewide Research - Freshwater Fisheries

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ANNUAL PROGRESS REPORT

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JOB PROGRESS REPORT

STATE: South Carolina PROJECT NUMBER: F- 63

PROJECT TITLE: Fisheries Investigations in Lakes and Streams - Statewide

STUDY: Survey and Inventory STUDY TITLE: Fishery surveys - Statewide Fisheries Research

JOB NO: II JOB TITLE: Relative performance of two strains of largemouth bass in farm ponds

Summary

During the project period July 1, 1999 - June 30, 2000 final analysis for the growth portion of this study was completed. Results were compiled into a manuscript which is currently under review for publication. That manuscript is included here as Appendix 1.

In June of 2000 N=26-30 juvenile largemouth bass were collected from 12 study ponds in a continuing effort to monitor the shift in allele frequencies in these study populations. These fish were shipped to Auburn University for genetic analysis along with juveniles that were collected in 1999. Results are pending, and will be reported when available

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Appendix 1.

A Comparison of First and Third Year Growth of Two Genetic Strains of Largemouth Bass When Stocked in Different Regions of South Carolina

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Abstract

A statewide reciprocal transplant study was initiated to compare the performance of two strains of largemouth bass endemic to South Carolina. South Carolina is located in the broad hybrid zone that exists between the ranges of the northern and Florida subspecies of largemouth bass. Allozyme surveys have shown South Carolina coastal largemouth bass populations possess 98% Florida alleles, while Piedmont populations possess as few as 36% Florida alleles. Thirty seven new or renovated farm ponds were stocked in 1994 and 1995 with either coastal or Piedmont strain largemouth bass. We characterized performance differences between the two strains by evaluating growth of original stocks at one and three years. Selected water quality parameters were monitored to define differences among ponds. Region (Coastal Plain or Piedmont), strain, and the interaction of region and strain were tested as predictors of growth rate for first year and third year growth. Differences between regions were significant (P=0.05) for growth at age-1 and at age-3, with fish stocked in the Coastal Plain growing faster. Differences due to strain and the region/strain interaction were not significant.

Introduction

Two subspecies of largemouth bass *Micropterus salmoides,* the Florida *M. s. floridanus* and the northern largemouth bass *M. s. salmoides,* exist and readily interbreed in both natural and hatchery environments (Isely et al., 1987, Gilliland and Whitaker 1989, Philipp and Witt 1991). The range of the Florida subspecies (FLMB) is restricted to peninsular Florida. The northern subspecies (NLMB) is found in the Mississippi drainage and the Atlantic Slope coastal drainage, north of Maryland (Philipp et al., 1983).

South Carolina is located in the broad hybrid zone between the ranges of the two pure subspecies. A statewide allozyme study of largemouth bass confirmed that South Carolina populations were hybrids (Bulak et al., 1995). This study also showed the existence of a geographic cline within South Carolina where the relative abundance of Florida alleles decreased from southeast to northwest. The relative frequency of alleles that were diagnostic for the Florida subspecies ranged from 98% in Lake Moultrie, a Coastal Plain reservoir, to 36% in Lake Wateree, a Piedmont reservoir.

Physiological and ecological differences among FLMB, NLMB, and their hybrids have been documented. A number of studies have shown a difference in the response to various temperature regimes (Fields et al., 1987, Carmichael et al., 1988). Other studies have shown differences in timing of spawning, growth rate, reproductive success and survival of the two subspecies (Philipp and Witt 1991, Maceina et al. 1988, Gilliland and Whitaker 1989, Isely et al. 1987).

The objective of this study was to examine growth differences between Piedmont (Lake Wateree) and coastal (Lake Moultrie) strains of largemouth bass in South Carolina. Privatelyowned ponds were used as study sites. Each pond was stocked with either a coastal or Piedmont strain of largemouth bass. The objective was assessed by measuring growth to age-1 and age-3.

Materials and Methods

Ponds were selected prior to stocking through a series of phone interviews and site visits. All ponds measured 0.4 to 1.2 ha and were either new or recently renovated. Ponds were located in either the Coastal Plain or Piedmont regions of South Carolina. All study sites were relatively secluded and showed little potential for invasion by wild fish. Finally, all pond owners agreed to allow site access to study personnel for data collection.

Largemouth bass for experimental stockings were produced from fish collected from Lakes Moultrie and Wateree. Lake Moultrie broodfish were collected by electrofishing in March of 1993. Lake Wateree broodfish were collected by electrofishing in March of 1994. Stocks were held in separate ponds. In 1994 and 1995 the resulting fry from each strain were collected and transferred to grow-out ponds where they were raised to a total length of approximately 25 mm. Fry were harvested from as many schools as possible to maximize the number of parents contributing to the gene pool.

Size at stocking and allele frequencies characteristic of the northern and Florida subspecies were determined for each strain. At harvest, forty fingerlings from each strain were weighed (gm), measured (TL mm) and then preserved in 100% isopropyl alcohol. Also, two sets of 100 fingerlings from each strain were placed on dry ice and stored frozen for allozyme analysis. Horizontal starch gel electrophoresis was performed according to Norgren (1986). Gels were stained for two allozymes (*sAAT-2**, *sIDHP-2**), with fixed allelic differences and two with non-fixed differences (*sMDH-B**, *sSOD-1**) between the northern and Florida subspecies. Allele frequencies of stocked fingerlings were compared to source lake populations (as defined in Bulak et al. 1995) using the G-test (Sokal and Rohlf, 1969).

One half of the ponds in each region were stocked with Moultrie and the other half with Wateree strain bass. Ponds were chosen at random for stocking with the Lake Moultrie strain. As each pond was chosen, its closest neighbor was assigned the Wateree strain. This ensured a uniform distribution of each strain throughout each region. Only one strain was hauled per day and the truck was flushed and stocked with fresh fingerlings each morning. Largemouth bass were hand counted and stocked at the rate of 124 and 247 fingerlings per hectare for unfertilized and fertilized ponds, respectively.

To account for productivity differences among ponds, selected water quality parameters were measured. Water quality was measured three times in 1994 and twice a year in 1995-1997, during the early summer to early fall growing season. Hardness and alkalinity were measured using a standard Hach kit with digital titrator. Temperature and pH were measured using an Orion field pH meter equipped with a Ross electrode. Water samples for chlorophyll-a determination were taken from 0.3 m below the surface at three sample sites on each pond. Sample sites followed the pond's stream gradient with an upper or inflow site, a middle, and a lower or outflow site. Chlorophyll-a concentration was determined with a Turner Filter Fluorometer Model 111 using the methods outlined in Arar and Collins (1992) for calibration and sample analysis.

Mean annual water quality parameters were computed for each pond. Mean pH, hardness, and alkalinity were the simple average of measurements taken throughout the sampling season . Mean annual chlorophyll-a concentration was computed by first taking the mean of the three samples for each sampling event and then taking the average of these means for each pond.

Adult largemouth bass were collected by electrofishing or angling from each pond at one and three years post-stocking. Ponds stocked in 1994 were sampled from 6/15-7/27/95 and from 6/12-8/21/97. Ponds stocked in 1995 were sampled from 6/11-6/19/96 and from 6/1-6/26/98. For the assessment of age-1 growth, we collected 10% of the number stocked with a minimum of 20. All fish were weighed, measured, and returned to the pond. Scales were collected from fish that were suspiciously large or small for age verification. To assess growth to age-3, we collected as many bass as possible during each site visit. All collected fish were weighed, measured and fin-clipped, to avoid re-sampling. A length-frequency histogram was constructed in the field so that apparent age classes could be visualized. Scales were taken for age estimation from some fish from each size group, and from all fish that appeared to be older than age-1. In 1998, all fish in the largest size class and several from smaller size classes were sacrificed; otoliths, as well as scales were collected from these fish. Age was estimated from scales and otoliths, where available, by two independent readers. Growth rate for each fish was computed as:

$$\text{growth rate} = \frac{\text{length at harvest - length at stocking}}{\text{days since stocking.}}$$

Mean growth rate at age-1 and age-3 of largemouth bass was computed for each study pond. Atypical ponds were identified and not included in analysis of growth. These included ponds where introductions of wild fish or poor water quality had a substantial effect on reproduction or forage availability.

A mixed linear model (SAS, 1996) was used to identify factors that were significant predictors of largemouth bass growth rate. Region (Piedmont or Coastal Plain) and strain were fixed effects while individual study sites (pond) were random effects. The effects of pond , region, strain, and the interaction of region and strain were evaluated. Each water quality variable was included in the model as a covariate. Least squares analysis (SAS, 1996) was used to test the significance of the evaluated factors to growth rate. All statistical evaluations were conducted at P = 0.05.

Results

Thirty seven ponds were stocked in May of 1994 and 1995. In each geographic region, approximately half of the ponds were stocked with Wateree and half with Moultrie strain bass

Moultrie and Wateree strain bass were of similar size at stocking in both 1994 and 1995. In 1994, Moultrie fingerlings (N=41) averaged 26 mm TL (SD=3.3) while Wateree fingerlings (N=39) averaged 34 mm TL (SD=1.8). In 1995, Moultrie fingerlings (N=44) averaged 32 mm TL (SD=3.9) while Wateree fingerlings (N=40) averaged 25 mm TL (SD=2.7).

Allele frequencies of stocked fingerlings were generally consistent with source populations (Table 1). Lake Moultrie fingerlings were not significantly different from wild Lake Moultrie stock at any of the four loci examined in either 1994 or 1995. Lake Wateree fingerlings produced in 1994 from Lake Wateree brood stock were significantly different from the source population at *sMDH-B** and potentially at *sIDHP-2** . At *sMDH-B**, the stocked fingerlings possessed the northern allele in significantly higher numbers than the wild stock. Analysis at *sIDHP-2** indicated that stocked fingerlings possessed a rare allele, *sIDHP-2*142,* in significantly higher numbers than wild Lake Wateree stock. However, the presence of this rare allele in the 1994 stock was not confirmed; neither a survey of the wild stock or juveniles produced in 1995 and 1996 showed this rare allele. Lake Wateree fingerlings produced in 1995 were significantly different from their source population at *sAAT-2** and *sIDHP-2**. At *sAAT-2** the stocked fingerlings possessed the Florida alleles in significantly higher numbers than the wild stock. At *sIDHP-2** the stocked fingerlings possessed the northern allele in significantly higher numbers than the wild Lake Wateree stock. Despite these differences from their source, Wateree strain fingerlings still possesed a significantly greater percentage of alleles typical of the northern subspecies than did Moultrie strain fingerlings.

Water quality was variable among the study ponds (Table 2). The range of water quality values detected during the study were typical of South Carolina ponds.

Age-1 largemouth bass were collected from 38 of 40 ponds sampled in 1995 and 1996. Growth of individual fish was computed 386 to 474 days post-stocking.

Largemouth bass stocked in Coastal Plain ponds grew faster to age-1 (0 = 0.61 mm/d, SD = 0.11, N = 215) than those stocked in Piedmont ponds (0 = 0.55 mm/d, SD = 0.09, N = 324) (Figure 1). Mixed model analysis showed that region and pH, as a covariate, were significant predictors of age-1 growth. Least squares means analysis indicated the difference in growth to age-1 between regions was significant; there was not a significant difference between growth rates of the two strains or between the interaction of strain and region. Data from five atypical ponds were removed from the data set prior to this analysis.

Samples to assess growth to age-3 were collected from 35 of 36 ponds in 1997 and 1998. A total of 240 fish were aged; 57 age-3 largemouth bass were identified. Agreement between scales and otoliths for 54 fish was 65%. Growth was computed 1107 to 1197 days post-stocking.

There was a significant difference in growth to age-3 between regions (Figure 2.). Largemouth bass stocked in the Coastal Plain grew more (0 = 0.31 mm /d, SD = 0.04, N = 29) than those stocked in the Piedmont (0 = 0.27 mm per day, SD=0.04, N=28). Mixed model analysis showed that region was a significant predictor of growth to age-3. Least square mean analysis confirmed a significant difference in growth between regions. Strain was not a significant predictor of age-3 growth.

Discussion

This study documented that when evaluating largemouth bass strains endemic to South Carolina, the region where fish were stocked was the most important predictor of their growth. Largemouth bass of both strains exhibited significantly greater growth in Coastal Plain ponds than in Piedmont ponds. This is likely because fish stocked in the Coastal Plain experienced a milder climate and longer growing season than those stocked in the Piedmont. For example, Greenwood, a Piedmont town, has a mean annual temperature of 15.6°C while Moncks Corner, a town in the Coastal Plain, has a mean annual temperature of 17.6°C.

Genetic strain did not have a significant impact on growth in this study, neither whithin the two geographic regions nor statewide. In a reciprocal transplant study in Illinois, Phillip and Claussen (1995) found that largemouth bass from a northern river drainage differed significantly from fish from a southern river drainage with respect to growth, survival and reproductive success. Each strain performed best in its native region. This indicates that local adaptations can result in demonstrable differences between largemouth strains even of the same subspecies, and even when those strains are geographically close. The largemouth bass strains we evaluated in South Carolina were from close geographic regions but were quite divergent genetically. Still we did not observe any difference in growth between them.

High environmental variability among ponds, and small sample sizes of age-3 bass may have impacted our ability to detect growth differences between strains. A study design where ponds were stocked with equal numbers of fish from each strain would have minimized the effect of pond to pond variation. We have employed this strategy in an ongoing effort. Unanticipated difficulty in collecting 3 year olds could have been avoided by total sampling (i.e. draining and rotenone renovation) of each pond. This was not considered due to the private ownership of each pond site.

The lack of growth differences between these two strains indicates that small pond owners and managers in South Carolina probably can not predictably impact, at least in the short term, the success of their fishing ponds by stocking a particular strain of largemouth bass. This should not be used to infer a lack of fitness differences between the two strains studied**.** Bulak et al. (1995) proposed that the largemouth bass allelic cline in South Carolina was maintained by a natural selection gradient**.** Other factors related to the fitness of a fish, such as disease resistance and reproductive timing, were not evaluated in this study. There may also be differences in growth that would show up in older age classes.

In a continuation of the present study, we will monitor the allele frequencies of filial generations of largemouth bass produced in the study ponds. Changes in allele frequencies over time will provide direct information as to what genotypes are most successful in each region. In recent years South Carolina has adopted a regionalized approach to stocking largemouth bass.

We recommend continuing the current policy to protect the existence of potentially important local adaptations.

Acknowledgments

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Table 1. Allele frequencies for Moultrie and Wateree strain largemouth bass fingerlings used to stock study ponds in 1994 and 1995, with survey data of allele frequencies for L. Moultrie and L. Wateree where stocks originated. Alleles, or allele pairs, listed first are fixed (sAAT-2*, sIDHP-2*) or dominant in the Northern subspecies. Alleles listed second are fixed or dominant in the Florida subspecies. An * indicates a significant difference (P=.05) from survey data.

	Lake Moultrie			Lake Wallace		
Locus/allele	1995 survey data	1994 fing	1995 fing	1995 survey data	1994 fing	1995 fing
	N=116	N=52	N=100	N=122	N=100	N=100
*sAAT-2**						
100, 110	0.10	0.19	0.14	0.66	0.65	0.44*
126, 139	0.90	0.81	0.86	0.34	0.35	0.54*
*sIDHP-1**						
100	0.02	0.00	0.02	0.47	0.18*	0.66*
121	0.98	1.00	0.98	0.52	0.50*	0.34*
142	0.00	0.00	0.00	0.01	0.32*	0.00*
*sMDH-B**						
100	0.00	0.00	0.00	0.60	0.73	0.60
114	1.00	1.00	1.00	0.40	0.27	0.40
*sSOD-1**						
147	0.19	0.14	0.13	0.57	0.58	0.64
100	0.81	0.86	0.87	0.43	0.42	0.36

Table 2. Water quality parameters monitored on study ponds, with mean, standard deviation and range reported for each. Mean values reported are for the three year sampling period.

	Parameter			
	chl-a (µg/l)	pH	hardness (mg/l as $CaCO_3$)	alkalinity (mg/l as $CaCO_3$)
N	42	42	42	41
Mean	5.3	7.6	38.1	34.1
Standard Dev.	2.1	0.9	32.2	27.0
Range	2.2 - 10.4	5.3 - 9.8	3.2 - 172.8	3.3 - 137.2

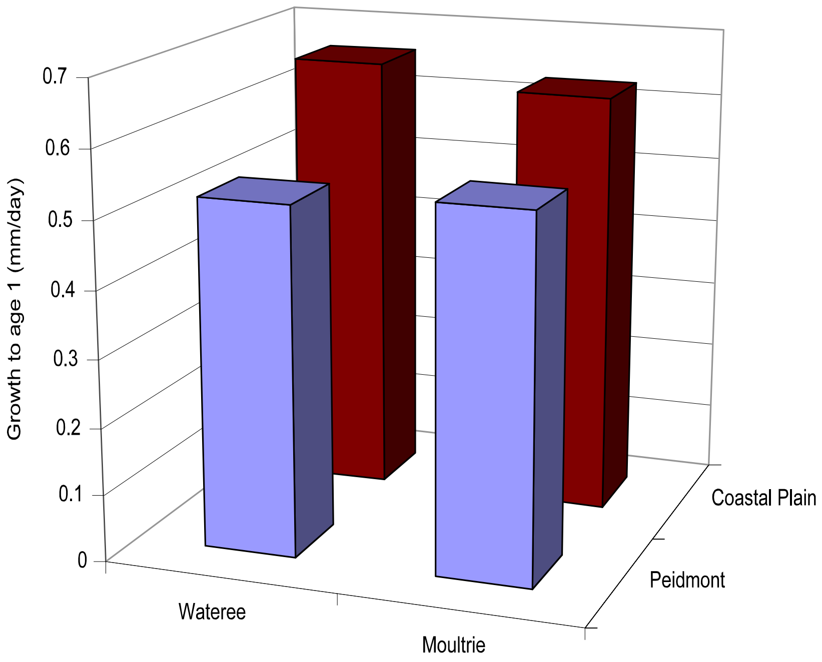

Figure 1. Growth to age 1 of largemouth bass in mm/day. Results are presented for each of four study groups defined by region (Coastal Plain or Piedmont) and strain (Moultrie or Wateree).

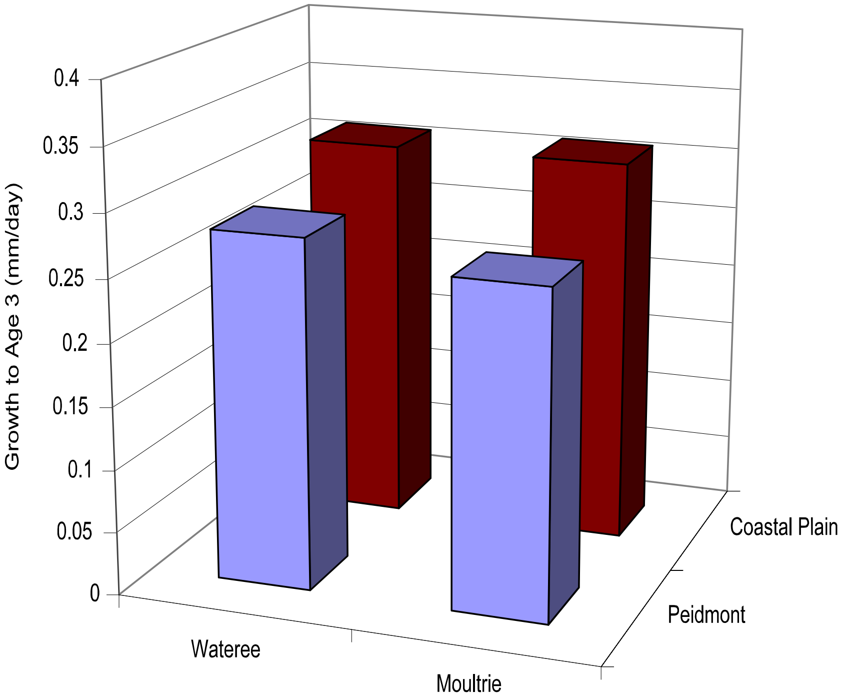

Figure 2. Growth to age 3 of largemouth bass in mm/day. Results are presented for each of four study groups defined by region (Coastal Plain or Piedmont) and strain (Moultrie or Wateree).

JOB PROGRESS REPORT

STATE: South Carolina PROJECT NUMBER: F- 63

PROJECT TITLE: Fisheries Investigations in Lakes and Streams - Statewide

STUDY: Survey and Inventory STUDY TITLE: Fishery surveys - Statewide
Fisheries Research

JOB NO: II JOB TITLE: Relative performance of two strains of largemouth bass in state lakes

Introduction

Two subspecies of largemouth bass *Micropterus salmoides*, the Florida largemouth bass *M. s. floridanus* and the northern largemouth bass *M. s. salmoides*, exist and readily interbreed in both hatchery and reservoir environments (Isely et al., 1987, Gilliland and Whitaker 1989, Philipp and Witt 1991). The native range of the Florida subspecies (FLMB) is restricted to peninsular Florida. The northern subspecies (NLMB) is native to waters north along the Atlantic coast states from Maryland and west to the Mississippi (Philipp et al., 1983).

South Carolina is located in the broad hybrid zone between the ranges of the two subspecies. A statewide allozyme study of largemouth bass confirmed that South Carolina populations were hybrids (Bulak et al., 1995). This study also showed the existence of a geographic cline within South Carolina where the relative abundance of alleles typical of the Florida subspecies decreased from southeast to northwest. The relative frequency of alleles that are fixed for the Florida subspecies ranged from 98% in Lake Moultrie, a Coastal Plain reservoir, to 36% in Lake Wateree, a Piedmont reservoir. It was suggested that natural selection played a role in maintaining this allelic cline.

Physiological and ecological differences among FLMB, NLMB, and their hybrids have been documented. A number of studies have shown a difference in the response of the FLMB, NLMB, and their hybrids to various temperature regimes (Fields et al., 1987, Charmichael et al., 1988). Other studies have shown differences in timing of spawning, growth rate, reproductive success and survival of the two subspecies (Philipp and Witt 1991, Maceina et al. 1988, Gilliland and Whitaker 1989, Isely et al. 1987).

The objective of this study was to examine performance differences between Lake Wateree and Lake Moultrie genetic strains of largemouth bass found in South Carolina. Two newly renovated state owned lakes, Wallace and Sunrise, were stocked with largemouth bass fingerlings from each strain. Strains were produced on separate hatcheries from broodfish collected from Lakes Wateree and Moultrie. Each strain received either a single or double oxytetracycline mark prior to stocking. Lakes Wallace and Sunrise were stocked with equal proportions of each strain. The objective will be achieved by measuring growth of stocked bass at age-1 and age-3 and by monitoring the long term temporal change in juvenile genotypes.

Methods

Sunrise Lake, a 20 acre lake in Lancaster County, and Lake Richard B. Wallace, a 280 acre lake in Marlboro County, were renovated during the summer of 1996. Largemouth bass for experimental stockings were produced from adult bass collected from Lakes Moultrie and Wateree. Lake Moultrie broodfish were collected by electrofishing in March of 1993 and were housed separately from other stocks at Cheraw State Fish Hatchery. Lake Wateree broodfish were collected in early Spring of 1997 and transported to Cohen Campbell Fisheries Center where they were stocked directly into a spawning pond separate from other stocks. Each group of broodfish was allowed to spawn. Resulting fry were harvested from as many schools as possible to maximize the number of parents contributing to the gene pool, and were grown out to fingerlings.

Prior to stocking fingerlings from each strain were marked by immersion for 6 hours in a 500 ppm solution of oxytetracycline. Moultrie strain largemouth bass were double marked, first on 4/16/97 as fry, and then on 5/5/97 as fingerlings. Wateree strain largemouth bass were single marked as fingerlings on 4/25/97.

Each lake was stocked with equal numbers of each strain at the rate of 100 fish per acre in April and May of 1997. Lake Wallace was stocked with 28,000 and Sunrise Lake with 2000 largemouth bass. (Lakes were stocked in October 1996 with a combination of bluegill *Lepomis macrochirus* and redear *L. microlophus* fingerlings at the rate of 1000 per acre.) Wateree strain fingerlings were stocked on 4/25/97. Moultrie strain fingerlings were stocked on 5/5/97. Total lengths were recorded for a sample of 100 fingerlings from each strain at time of stocking. One hundred additional fingerlings from each strain were transported to the Berry's Mill Hatchery near Traveler's Rest and held in separate ponds for use in mark evaluation and genetic analysis.

Ponds at Berry's Mill were harvested on 11/6/97 and sagittal otoliths, liver, and muscle tissue were collected from each individual. Known single and double marked otoliths were randomly coded and given to an experienced reader for evaluation. Otoliths were mounted, sectioned and polished to the core. Presence or absence of a mark on the otolith was determined with a flourescent compound microscope.

Liver and muscle tissues were stored at -80°C for genetic analysis. Horizontal starch gel electrophoresis was performed according to Norgren (1986). Gels were stained for four enzymes which are diagnostic for the Florida and northern subspecies of largemouth bass. These are aspartate aminotransferase (*sAAT-2**), isocitrate dehydrogenase (*sIDHP-1**) and superoxide dismutase (*sSOD-1**) from liver tissue, and malate dehydrogenase (*sMDH-B**) from muscle tissue. Alleles typical of the northern subspecies are *sAAT-2*100* and *sAAT-2*110*, *sIDHP-*

*1*100, sMDH-B*100,* and *sSOD-*147.* Alleles typical of the Florida subspecies are *sAAT-2*126* and *sAAT-2*139, sIDHP-1*121*, *sMDH-B*114,* and *sSOD-1*100.* A genetic baseline was determined for Lakes Moultrie and Wateree using data from an initial statewide survey (Bulak et al., 1995) and data collected from large and small fish for a related performance study. Allele frequencies of each stock was compared to baseline genetic data for source populations using the G-test (Sokal and Rohlf, 1969).

Lakes were sampled in the Spring and Summer of 1998 for collection of juveniles and age-1 adults, in Summer of 1999 for collection of juveniles, and in Summer of 2000 for collection of juveniles and age-3 adults. Adults were collected by electrofishing from Lake Wallace on March 31 and April 4, 1998, and on May 25, 2000. Adults were collected from Sunrise Lake on May 22, 1998, June 1, and August 3, 2000. Total length and weight were recorded for each individual. Sagittal otoliths were collected from each largemouth bass and stored in the dark until processed for mark determination. Liver and muscle tissues were collected from age-1 fish and stored at -80°C for genetic analysis.

Seining for juveniles was conducted on both lakes in the early summer of 1998, 1999 and 2000. A variety of areas and habitats were sampled. An attempt was also made to collect young of the year from Lake Wallace in the fall of 2000 by electrofishing.

Otoliths collected from adult largemouth bass were mounted, sectioned, and polished to the core for mark determination. Marks were evaluated by two independent readers using a flourescent compound microscope. Otoliths were determined to be single marked, double marked or unmarked by each reader. Those otoliths that were not agreed on after consultation were thrown out. Growth at age-1 and age-3, in mm/day, was compared for Moultrie strain and Wateree strain fingerlings in each lake using the T-test. Length frequency distributions were generated for each strain and were compared using the Kolmogorov-Smirnov 2-sample test.

Results

Size at stocking was similar for the Moultrie and Wateree strains. Moultrie strain fingerlings averaged 24.4 mm total length (n = 102, std = 2.6). Wateree strain fingerlings averaged 23.3 mm total length (n = 92, std = 6.2).

Mark evaluations were completed on a set of 68 otoliths. Because of questionable origin made evident by genetic analysis, 8 sets of otoliths were thrown out. Of 27 Wateree strain fish 100% were correctly identified. Of 33 Moultrie strain fish 91% were correctly identified.

Genetic analysis was completed for hatchery fingerlings of each strain, and comparisons made with historic data from wild stocks (Table 1.). Fingerlings of the Wateree strain were similar to the wild Wateree stock at three of four loci. However, at the *sIDHP-1** locus the Wateree strain fingerlings possessed significantly (p=0.05) more of the *sIDHP-1*100* allele which is typical of the northern subspecies. Fingerlings of the Moultrie strain differed markedly from wild lake Moultrie stock at three of the four loci examined. They possessed significantly more of the *sAAT-2*100,110* alleles, the *sIDHP-1*100* allele, and the *sMDH-B*100* allele, all typical of the northern subspecies.. Fingerlings of the Moultrie strain possessed *sMDH-B*100* at a frequency of 20% although broodstock from Lake Moultrie were known to be fixed for *sMDH-B*114.*

Those fish possessing the *sMDH-B*100* allele were also found to be single rather than double marked. This poses a problem, as they are undistinguishable, both genetically and by mark, from the Wateree strain fish. For the purposes of this report, all single marked fish are considered to be of the Wateree strain.

Age-1 largemouth bass were collected by electrofishing from Lake Wallace on 4/31/98 and 5/22/98. Fish averaged 274.1 mm total length (n = 104, std = 28.2) and weighed an average of 359.3 g (n = 104, std = 123.5) Age-1 largemouth bass were collected from Sunrise Lake on 5/22/98. These fish averaged 235.7 mm total length (n = 92, std = 17.3) and weighed an average of 171.7 g (n = 92, std = 49.8).

Table 1. Allele frequencies (proportions) for largemouth bass used to stock study lakes, with historic data for reservoirs where stocks originated. A + indicates allele frequencies significantly different from survey data.

	Lake Wateree		Lake Moultrie	
Locus/Allele	Historic Data	1997 Fing.	Historic Data	1997 Fing.
sAAT-2*				
100, 110	146 (0.66)	26 (0.69)	47 (0.10)	16 (0.23) +
126, 139	74 (0.34)	12 (0.31)	443 (0.90)	54 (0.77) +
sIDHP-1*				
100	116 (0.48)	37 (0.69) +	11 (0.02)	12 (0.16) +
121	124 (0.52)	17 (0.31) +	455 (0.98)	64 (0.84) +
sMDH-B*				
100	141 (0.61)	39 (0.70)	0 (0.00)	16 (0.20) +
114	91 (0.39)	17 (0.30)	494 (1.00)	64 (0.80) +
sSOD-1*				
147	143 (0.57)	29 (0.54)	82 (0.19)	17 (0.24)
100	107 (0.43)	25 (0.46)	344 (0.81)	55 (0.76)

Clear marks were detected on 49 of 104 otoliths sampled from Lake Wallace, and on 44 of 92 otoliths sampled from Sunrise Lake. Twenty-one percent of otoliths from Lake Wallace were determined to be unmarked, and 32% were not readable due to cracks or occlusions. From Sunrise Lake 22% of otoliths were read as unmarked and 29% were not readable.

Marked fish were identified to strain (1 mark = Wateree, 2 marks = Moultrie), and growth rate by strain was computed for each lake (Table 2). Differences in growth to age-1 between the two genetic strains were tested for each lake using the T-test and were not significant.

Age-3 largemouth bass were collected from Lake Wallace on May 25, 2000. Fish averaged 414.8 mm total length (n=40, std=17.1) and weighed an average of 1249.9 g (n=40, std=213.1). Mark evaluations were completed. Of 40 age-3 largemouth bass collected 11 (27%) were of the Wateree strain, 28 (70%) were of the Moultrie strain, and 1 was not readable. Growth to age-3 was computed for each strain. Differences in growth between the two strains were tested using the T-test and were not significant (Table3). Length frequency distributions for each strain were generated (Table 4). Differences between the two distributions were tested using the Kolmogorov-Smirnov 2-sample test and were not significant, although the 8 largest fish collected were of the Lake Moultrie strain.

Table 2. Mean growth rate at age-1, in mm/day, for Moultrie and Wateree strains of largemouth bass stocked in Lake Wallace and Sunrise Lake with corresponding T-test statistics and probabilities.

	Lake Wallace			Sunrise Lake		
Strain (N)	Rate (mm/d)(N)	T	Prob>|T	Rate (mm/d)	T	Prob>|T|
Moultrie	0.75 (13)	1.29	0.2038	0.54 (19)	-0.64	0.5245
Wateree	0.72 (31)			0.55 (30)		

Table 3. Mean growth rate at age-3, in mm/day, for Moultrie and Wateree strains of largemouth bass stocked in Lake Wallace with corresponding T-test statistics and probabilities.

		Lake Wallace		
Strain	N	Rate (mm/day)(std)	T	Prob>T
Moultrie	28	0.34 (0.01)	-0.97	0.3342
Wateree	11	0.35 (0.02)		

Table 4. Length frequency distributions by genetic strain for age-3 largemouth bass collected from Lake Wallace.

	Frequency by strain	
length group (mm)	Moultrie	Wateree
380	1	1
390	3	1
400	7	3
410	8	2
420	1	3
430	3	1
440	4	0
450	1	0

Largemouth bass were collected in 2000 from Sunrise Lake June 1 during the day and August 3 at night. Eight age-3 fish were collected. They averaged 437.9 mm total length (std=34.7) and weighed an average of 1148.5 g (std=319.9). Because of the small sample size these fish have not been evaluated yet for marks. This lake is scheduled for a major drawdown for repairs to the dam. Plans are to make another attempt at collecting age-3 largemouth bass this winter while the lake is low.

Despite efforts to sample a variety of areas and habitats, no juvenile largemouth bass were collected from either lake in 1998, nor from Lake Wallace in 1999 and 2000. Thirty juvenile largemouth bass were collected from Sunrise Lake in 1999 and 2000. These fish have been sent to the South Eastern Fisheries Genetics Cooperative at Auburn University for genetic analysis.

Discussion

The marked genetic difference between Moultrie strain fingerlings and Lake Moultrie broodfish is a concern, especially at the *sMDH-B** locus. It indicates that not all of the fingerlings stocked as Moultrie strain were produced from Lake Moultrie broodfish.

When they were collected in 1993 all Lake Moultrie broodfish underwent liver and muscle biopsies. Tissues were analyzed so that the alleles expressed at each loci for every fish was known. None of 112 fish biopsied possessed the *sMDH-B*100* allele. Eight out of 40 Moultrie strain fingerlings were homozygous for *sMDH-B*100* meaning they inherited that allele from both parents. All other fingerlings were homozygous for *sMDH-B*114.* The presence of the northern allele and lack of heterozygotes indicate that the fish possessing the northern allele were spawned in a different pond and from a group of parents other than the Lake Moultrie broodfish.

Fish possessing the *sMDH-B*100* allele also possessed a different oxytetracycline mark from other Moultrie fingerlings. Moultrie fingerlings were marked twice, first as fry when harvested from the spawning pond, and then as fingerlings when taken from the hatchery for stocking. All eight of the fish homozygous for *sMDH-B*100* had only the later mark.

There are a number of possible explanations for the presence of the fish homozygous for *sMDH-B*100*. The first is that the Moultrie strain fingerlings were contaminated on the hatchery. This would have occurred sometime after the marking of fry but prior to the second marking, with the source of contamination either in the grow out pond or the fish house.

A second explanation is that the Moultrie strain fish were contaminated in the holding pond at Berry's Mill with fish of the single marked Wateree strain. The two strains were housed in adjacent ponds separated by an earthen dike. A third explanation is that the samples collected from Berry's Mill were mishandled and some Wateree strain fish were improperly coded as Moultrie strain. The probability that 8 fish chosen at random from the Wateree strain will all be homozygous for *sMDH-B*100* is P = 0.002.

There is also the possibility that genetic and/or otolith interpretations of the known stocks were incorrect. This will be further investigated by reviewing those otolith samples and genetic records.

If the Moultrie strain fingerlings were in fact contaminated prior to stocking, the effects on the experiment can be assessed. Our experimental design called for the lakes to be stocked with equal proportions of each strain. Performance would be assessed by measuring growth of stocked fish at age-1 and age-3, and by the long term monitoring of allele frequencies of subsequent year classes.

In fact, the lakes were stocked with 50% Wateree strain fingerlings, 40% Moultrie strain fingerlings, and 10% fingerlings of unknown origin. Because the fingerlings of unknown origin are single marked they are indistinguishable from fish of the Wateree strain. Of the marked fish collected from lakes Wallace and Sunrise, 61% and 70% respectively were single marked. Growth assessments of the Wateree strain include those fish of unknown origin. Assessment of reproductive success of the Moultrie and Wateree strains by following changes in allele frequencies of subsequent generations will be difficult because of the unbalanced stocking, and the inability to quantify the contribution of the unknowns.

While these factors negatively impact our ability to draw conclusions regarding the performance of the Moultrie and Wateree strains, valuable information can still be obtained. Genetically the 8 unknown fish are similar to the Wateree strain. Though as a group they possess more northern alleles, individually they are not distinguishable from a Wateree strain fish. Growth can still be compared between the Moultrie strain and the more northern, single marked fish.

Comparison of growth at age-1 do not show significant differences between the strains for either lake. Larger sample sizes would increase our ability to detect differences. Although about 100 fish were collected from each lake, only about half of these are included in analysis. A number of otoliths examined were either unmarked, or marked but too difficult to read because the core was occluded by cracks. Those samples that were too difficult to read should be reexamined using the other otolith.

Comparison of growth at age-3 did not show any significant difference between strains in Lake Wallace. However, a look at the length frequency distribution showed us that the 8 largest fish collected were all of the Moultrie strain. Though the length frequencies also are not significantly different, we are concerned that our small sample size especially for the Wateree strain (N=11) has hindered our ability to detect differences. When this data set is tripled to include 117 fish differences in growth and length frequencies are significant.

Largemouth bass in Sunrise Lake grew much slower in their first year than those in Lake Wallace. While no water quality measurements were taken a visual inspection of the two lakes indicated they were managed quite differently. Lake Wallace appeared to have received more than adequate fertilizer applications; it was deep green with no visibility below the surface in some areas. Sunrise Lake was very clear throughout. If fertilizer applications were made at Sunrise Lake they were not effective. Both of these lakes were stocked at the fertilized rate of 1000 bream/100 bass per acre.

Recommendations

Continue study. Place emphasis on increasing sample size. Process otoliths from selected samples of age-1 fish and repeat analysis with larger sample size. Collect 100 largemouth bass from Lake Wallace in Spring/Summer of 2001 for growth comparison. Perform genetic analysis on year classes collected from Sunrise Lake. Continue to collect juveniles from Sunrise Lake every other year for long term evaluation of shifts in allele frequencies. Ensure that all state lakes are managed optimally with regard to liming and fertilization regimes.

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Prepared by: Jean K. Leitner Title: Fishery Biologist

JOB PROGRESS REPORT

STATE: South Carolina PROJECT NUMBER: F- 63

PROJECT TITLE: Fisheries Investigations in Lakes and Streams - Statewide

STUDY: Survey and Inventory STUDY TITLE: Fishery surveys - Statewide Fisheries Research

JOB TITLE: A genetic survey of smallmouth bass populations in South Carolina

Introduction

The smallmouth bass, *Micropterus dolomieu*, is native to the middle and upper Mississippi River basin. It has been widely introduced outside of its native range. It's North American distribution now includes the mountainous and Piedmont portions of the mid-Atlantic states and even the Coastal Plain where adequate habitat exists (Rohde et al, 1994). Smallmouth bass require clear running or deep water.

Two subspecies of smallmouth bass are recognized. *M. d. dolomieu* is the northern form. It is native to the area from the Missouri and Meramec river basins northward and east of the Mississippi River. *M. d. velox*, also called the Neosho subspecies, occupies a range restricted to direct tributaries of the middle Arkansas River in the far western and southern Ozarks.

Smallmouth bass are not native to South Carolina. They have been stocked fairly regularly in the state since the early 1980's. Fish are produced on two state hatcheries from stocks that we expect originated from the Ozark genetic strain. A number of introduced populations have been established. They include the upper Broad River and its tributaries in Cherokee county, Lake Jocassee in Oconee county, and Lake Keowee in Oconee and Pickens counties.

The objective of this study was to genetically survey several of our reproducing populations and our hatcheries, to see how they compare to each other, and to determine the level of genetic diversity present. We also wanted to see how closely related our hatchery stocks are to the Ozark strain of smallmouth bass from which they reportedly originated.

Methods

Smallmouth bass were collected from each of five populations by electrofishing, angling and gillnetting in the summer and fall of 1999. Fish were collected from Broad River and Kings Creek in Cherokee County, from Lake Jocassee in Oconee County, and from the Dennis Center and Cheraw state fish hatcheries. Total lengths were recorded for each fish. Liver, muscle and eye tissues were extracted from each fish and immediately placed on dry ice. Carcasses of fish from Broad River and Kings Creek were saved for future otolith extraction and analysis.

Tissue samples were shipped to Auburn University for genetic analysis at 20 enzyme loci. Samples were analyzed using horizontal starch gel electrophoresis according to the procedures of Steiner and Joslyn (1979), Philipp et al. (1982) and Norgren et al. (1986). Allele frequencies were computed and measures of genetic diversity were calculated for each population. These included mean number of alleles per locus, percentage of polymorphic loci and mean heterozygosity. Genetic relationships among all five South Carolina populations were calculated using Rogers' (1972) genetic similarity. A dendogram of these relationships was generated.

Results

Smallmouth bass (N=116) were collected from all populations sampled. Table 1 lists the number collected and mean lengths by population. Fish were examined electrophoretically at the 20 enzyme loci listed in Table 2. Allele frequencies were computed for the 10 loci found to be polymorphic (Table 3).

Table 1. Mean lengths for smallmouth bass collected from South Carolina populations in the Summer and Fall of 1999. Length data for Lake Jocassee is unavailable.

		Length (mm)		
Population	N	range	mean	sd
Broad River	32	72-391	184.3	83.4
Kings Creek	21	70-303	120.8	63.2
Lake Jocassee	8	-	-	-
Dennis Center	25	112-177	140.1	18.7
Cheraw	30	43-179	125.0	36.8

Table 2. Enzymes, loci, tissues (E=eye, L=liver, M=muscle) and buffers used for smallmouth bass genetics survey.

Enzyme	Number of loci	Enzyme number	Locus	Tissue	Buffer
Aspartate aminotransferase	1	2.6.1.1	AAT-1	L	EDTA
Alcohol dehydrogenase	1	1.1.1.1	ADH	L	EDTA
Glucose dehydrogenase	1	1.1.1.47	GDH	L	TC
Glucose-6-phosphate isomerase	2	5.3.1.9	GPI-A,B	M	EDTA
Lactate dehydrogenase	2	1.1.1.27	LDH-A,B	E	EDTA
Malate dehydrogenase	2	1.1.1.37	MDH-A,B	M	EDTA
Malic enzyme	1	1.1.1.40	MEP-1	M	TC
Tripeptide aminopeptidase	1	3.4.-.-	PEPB	E	TC
Pepdidase-C	1	3.4.-.-	PEPC	L	EDTA
Dipepdidase	1	3.4.-.-	PEPA	E	TC
Pepdidase-S	1	3.4.-.-	PEPS	L	TC
Phosphogluconate dehydrogenase	1	1.1.1.44	PGDH	L	TC
Phosphogluctomutase	1	5.4.2.2	PGM	M	EDTA
General protein	2	--	PROT-1,2	M	EDTA
Superoxide dismutase	1	1.15.1.1	SOD	L	EDTA
Triosephosphate isomerase	1	5.3.1.1	TPI	M	-------

Table 3. Allele frequencies for polymorphic loci in 5 populations of smallmouth bass in South Carolina.

	Populations				
Locus	Broad River	Cheraw	Dennis Center	Kings Creek	Lake Jocassee
AAT-1					
100	.475	.650	.140	.595	1.000
90	.525	.350	.860	.405	.000
ADH-1					
100	.333	.900	.760	.476	.625
53	.000	.000	.000	.024	.375
104	.667	.100	.240	.500	.000
GDH-1					
100	.405	.552	.480	.429	.375
86	.000	.086	.000	.048	.625
105	.595	.362	.520	.524	.000
GPI-A					
100	.976	1.000	1.000	.929	.167
76	.000	.000	.000	.000	.250
83	.000	.000	.000	.000	.167
216	.024	.000	.000	.071	.417
GPI-B					
100	1.000	.914	1.000	1.000	1.000
97	.000	.086	.000	.000	.000
MDH-A					
100	.976	1.000	1.000	.929	.438

80	.024	.000	.000	.071	.563

Table 3. (Cont'd)

	Populations				
Locus	Broad River	Cheraw	Dennis Center	Kings Creek	Lake Jocassee
MEP-2					
100	.143	.483	.540	.429	.750
92	.000	.069	.180	.190	.000
107	.476	.241	.200	.190	.000
111	.381	.155	.080	.143	.250
115	.000	.052	.000	.048	.000
PGM-1					
100	1.000	1.000	1.000	.881	.688
80	.000	.000	.000	.119	.250
60	.000	.000	.000	.000	.063
SOD-1					
100	.619	.650	.292	.548	.917
145	.357	.333	.708	.405	.000
210	.024	.017	.000	.048	.083
TPI-1					
100	.952	.828	1.000	.810	.438
86	.000	.000	.000	.095	.438
140	.048	.172	.000	.095	.063
194	.000	.000	.000	.000	.063

There was a large amount of genetic variation among and within these populations (Table 4). This is partly due to the examination of loci that we expected to be polymorphic. The hatcheries showed less variability than the wild populations, with the Dennis Center population much more homozygous than the others. Broad River, Kings Creek and Cheraw all had normal to high levels of variability. Lake Jocassee had extremely high levels of mean heterozygosity.

Population	Mean sample size per locus	Mean no. alleles per locus	Percentage of loci polymorphic	Mean Heterozygosity Direct/Expected
Broad River	20.9 (0.1)	1.7 (0.2)	53.3	.114 / .185 (.069) (.064)
Kings Creek	21.0 (0.0)	2.1 (0.3)	60.0	.086 / .246 (.030) (.068)
Lake Jocassee	7.7 (0.2)	1.9 (0.3)	53.3	.294 / .267 (.108) (.074)
Dennis Center	24.9 (0.1)	1.5 (0.2)	33.3	.033 / .146 (.023) (.059)

Table 4. Measures of genetic variability calculated for South Carolina smallmouth bass populations. All 20 loci examined are included in this measurement.

The dendogram generated for these five populations is shown in Figure 1. Populations were quite distinctive and genetic distances were relatively high. Broad River and Kings Creek were closely related. The Cheraw and Dennis Center stocks were in the same cluster but were more distantly related. The Lake Jocassee population was radically different from the other four populations; genetic distance was suggestive of a separate species or subspecies.

Figure 1. Genetic relationships among South Carolina smallmouth bass populations as calculated using Roger’s genetic similarity (1972).

```
                              Genetic Distance

.20       .17       .13       .10       .07       .03       .00
+----+----+----+----+----+----+----+----+----+----+----+----+


                                                         ****  Broad River
                                                    ******
                                                 ****    ****  Kings Creek

                                                 *  *
   ***********************************************  *********  Cheraw
   *                                             *
   *                                             ************  Dennis Center
   *
   **********************************************************  Lake Jocassee

+----+----+----+----+----+----+----+----+----+----+----+----+
.20       .17       .13       .10       .07       .03       .00
```

Discussion

Overall variability for the populations studied was high. This may be partly due to the enzyme loci examined. We purposefully selected loci that we expected would be useful in determining what genetic strains of smallmouth bass were present in South Carolina. Further evaluation is needed to determine if the lower variability at the Dennis Center is something that should be addressed.

The very large genetic distance between Lake Jocassee and the other populations is worthy of further study. Kings Creek, a tributary of the Broad River, is very closely related to the

Broad River population. Kings Creek and Broad River also cluster fairly closely with the hatcheries. Further distance between those four populations and Lake Jocassee would be expected because of at least two factors. There are dramatic differences in habitat between the lake and the streams, and the lake has not been stocked with hatchery fish in over ten years. Still, the genetic distance between Lake Jocassee and the other populations studied is much higher than expected and is consistent with that seen between some species.

Hybridization with redeye bass, *Micropterus coosae*, may have accounted for the high distance between the Lake Jocassee and other populations. Redeye bass are native to that system, and have been shown to successfully hybridize with smallmouth bass in the wild (Turner et al., 1991). Further evaluation of this smallmouth bass data together with recent data for South Carolina redeye bass may help show whether hybridization has occurred.

Further information is needed to complete the original goals of this effort. It is not clear whether the data from the hatcheries would indicate a need to increase diversity. We also do not have any information regarding the relationship of our fish with smallmouth bass of the Ozark strain. We will work with the staff at the South Eastern Fisheries Genetics Cooperative to get these questions, and those regarding possible hybridization, answered as clearly as is possible.

Recommendations

Continue data analysis. Use available data to investigate potential hybridization between smallmouth bass and redeye bass. Determine whether there is a need to increase diversity of the Dennis Center brood stock. Compare hatchery stocks to wild fish to determine if certain phenotypes are more successful in the wild. Compare populations to historic data for the Ozark strain of smallmouth bass. Collect additional smallmouth bass from Lake Jocassee to increase sample size.

Exercise caution in selection of stocking sites for non-native species. Consider all potential impacts on native fishes, including hybridization and competition for resources.

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STUDY COMPLETION REPORT

STATE:	South Carolina	PROJECT NUMBER:	F-63

PROJECT TITLE: Fisheries Investigations in Lakes and Streams - Statewide

SECTION TITLE: Survey and Inventory

STUDY : Development of Reservoir-Specific Largemouth Bass Management Models

Summary

During the project period July 1, 1999 - June 30, 2000 recent literature dealing with black bass management was reviewed. Spring electrofishing sampling data provided by the fisheries districts were reviewed and analyzed by reservoir, and estimates of parameters for recruitment, growth, and mortality of largemouth bass populations were extracted when sufficient data were available. Yield per recruit modeling was conducted for five reservoirs which encompassed the range of growth and mortality conditions observed in South Carolina; either a 356 or 404 mm minimum length limit maximized yield.

Introduction

The importance of largemouth bass to sport fishing in South Carolina is well known. A survey of freshwater fishermen commissioned by the South Carolina Wildlife and Marine Resources Department (SCWMRD), predecessor of the South Carolina Department of Natural Resources (SCDNR), in 1990 found that 28% of all fishermen fished for largemouth bass (Logan, 1990). Of fishermen who targeted a particular species, 37% fished for largemouth bass. According to a national survey conducted by the U.S. Department of the Interior et al. (1993), approximately 50% of resident and non-resident fishermen in South Carolina fished for black bass, primarily largemouth bass, in 1991. Logan (1990) reported that 48% of survey respondents felt that SCWMRD should pay more attention to the management of largemouth bass, and significant numbers supported harvest restrictions as management options.

Considerable effort is expended annually by district fisheries biologists in South Carolina to monitor the status of largemouth bass populations in reservoirs and streams. Techniques for conducting angler creel surveys, spring electrofishing and summer/fall cove rotenone sampling were standardized to facilitate the analysis and interpretation of data. Kirk (1989) summarized a decision-making process regarding management options that could follow from evaluation of the harvest potential of largemouth bass, based on data generated from standardized surveys and sampling. However, there are no definitive guidelines that management biologists must follow when making management recommendations.

Birth, growth, and death are dynamic processes which operate continuously and interactively on populations of living organisms. Population structure, however it is measured or expressed, is the cumulative result of these processes (each actually a rate function) at any point in time. Structural indices (age structure, length structure, relative condition) provide snap-shots which help to characterize the status of a population, but rate functions (recruitment, growth, and mortality) are needed to assess the dynamics of a population.

Historical spring electrofishing in South Carolina consisted primarily of the collection of largemouth bass length and weight data. Such data were useful for the computation of two structural indices: length structure and relative condition. Inferences were often made about recruitment and mortality from length structure representations and about growth from relative condition representations. However, rate functions can be estimated meaningfully only if the time step is known. Therefore, accurate and precise aging studies are essential elements of a sampling program.

In 1995 the Freshwater Fisheries Section of SCDNR approved a statewide management plan for black bass, including largemouth bass. Management goals were established to provide continuity and guidance to department personnel and the public, while the need for site-specific management authority was recognized. Having such guidelines would promote uniform, consistent assessments of black bass populations, and could enhance public understanding of and support for the process of managing the fishery. One goal common to all four species of black bass was to develop, maintain, and enhance the biological databases needed to make sound management decisions. Such databases can be used to define reservoir-specific management options, depending on the results of structured and objective assessment of a population.

While this agency still does not have a centralized database management system in place for freshwater fisheries, a step in that direction was taken during the first phase of this study (Bulak et al. 1998). A standardized protocol for collecting spring electrofishing data was approved and implemented, and a standardized data-entry program was distributed to each fisheries district. Data collected annually by the fisheries districts are now sent to the Fisheries Research Lab in Eastover for compilation and analysis using computer programs developed for that purpose. Current and historic data are then used to produce site-specific estimates of largemouth bass population parameters.

Accuracy in aging is extremely important in fisheries science and has critical implications for management. Age provides the time line upon which a number of rate functions, among them growth, mortality, and recruitment are based. In order to have a good understanding of the dynamics of a population, the underlying age information must be reasonably correct. Otherwise, significant misinterpretations of data can result. To ensure accurate aging of largemouth bass captured during spring electrofishing, we initiated an effort to standardize the otolith aging process and to establish a quality control procedure whereby ages determined by the Districts would be reviewed and verified (Bulak et al.1999).

The objective of the present study is to develop a quantifiable protocol for identifying and ranking management options in reservoirs through compilation, analysis, and interpretation of existing largemouth bass population data.

Materials and Methods

Spring electrofishing data collected in 1999 in accordance with the South Carolina Largemouth Bass Sampling Plan (SSP) were obtained from the districts and compiled and analyzed using programs developed previously. Metrics for recruitment, growth, and mortality were calculated for largemouth bass populations based on age assignments using combined 1997-99 age-length keys for each reservoir. Keys were applied to data collected during three years of spring electrofishing. Catch per unit effort (CPUE) of age-1 fish was used as an index of recruitment. CPUE was also computed in terms of length categories, using the five-cell model of Gabelhouse (1984). Stock density indicies (PSD, RSD-15, and RSD-20) were computed for each reservoir using the traditional method of Gabelhouse (1984) as described by Anderson and Neumann (1996). Annual mortality was estimated by catch curve analysis (Ricker 1975). Parameters of the Von Bertalanffy growth equation (Ricker 1975) were estimated using a beta version of Fishery Analyses and Simulation Tools (FAST) software, developed by J. W. Slipke and M. J. Maceina, Auburn University.

Yield per recruit analysis was used to evaluate bass fisheries in five reservoirs. FAST software was the modeling tool. Reservoir-specific data were used where available to set parameters for the model. Where data were not available, best estimates were used. Minimum length limits were evaluated.

Results and Discussion

Largemouth bass otoliths from seven reservoirs were obtained for confirmation of ages from Districts 2, 3, and 5 in 1999. Agreement with district-determined ages was high: in four reservoirs, it was 100%; in the other three, agreement ranged from 86-94%. Spring electrofishing data for 1999 were received from Districts 1, 2, 3, 4, and 5. Selected population parameters are summarized in Tables 1a-d for seven major reservoirs for which data were available.

Three years of standardized sampling on South Carolina's major reservoirs yielded estimates of growth, mortality, and recruitment. These estimates provided an initial assessment of management strategies in a yield-per-recruit simulation model. A paper describing this initial assessment was presented at the Black Bass 2000 Symposium, held in conjunction with the annual meeting of the American Fisheries Society in St. Louis, August 21-24, 2000. A draft of the paper, submitted for inclusion in the Proceedings of the Symposium, is included here as Appendix 1. Publication is pending.

Table 1a-d. Comparisons of largemouth bass population parameters in selected South Carolina reservoirs, 1999. Age-related parameters were computed from age frequency tables based on 1999 age-length keys, except for Lake Wateree, for which a 1998 age-length key was used.

1a. Mean total length (variance) in cm, by age.

Age	Keowee	Thurmond	Russell	Murray	Wateree	Marion	Moultrie
1	19.3 (2.69)	19.0 (1.58)	18.3 (1.67)	18.1 (3.72)	19.8 (1.29)	22.5 (3.34)	22.7 (2.86)
2	29.0 (1.77)	29.5 (0.92)	27.8 (1.11)	29.9 (3.07)	28.2 (1.70)	33.8 (2.57)	31.9 (1.97)
3	35.7 (1.34)	34.1 (0.94)	34.4 (0.94)	35.8 (3.15)	35.8 (1.58)	39.1 (2.31)	39.4 (0.66)
4	38.3 (1.82)	38.1 (1.15)	37.9 (1.53)	37.8 (1.70)	39.9 (0.67)	43.4 (5.55)	41.2 (0.77)
5	40.3 (1.51)				43.1 (1.52)		

1b. Catch per unit effort (no./hr) by age. Total includes fish older than 5.

Age	Keowee	Thurmond	Russell	Murray	Wateree	Marion	Moultrie
1	13.7	44.2	23.8	10.8	11.7	8.4	28.6
2	13.2	33.3	40.9	4.8	42.7	8.4	7.1
3	7.4	8.4	12.2	2.3	24.2	8.9	4.4
4	2.9	5.6	4.4	1.4	7.6	3.6	3.1
5	2.6	3.1	3.1	2.1	5.4	3.6	3.6
Total	43.9	97.8	86.9	24.4	101.2	44.9	56.4

Table 1a-d. Continued.

1c. Catch per unit effort (no./hr) by length category. Range of TL (mm) for each category is in parentheses.

Length Category	Keowee	Thurmond	Russell	Murray	Wateree	Marion	Moultrie
Prestock (<200)	6.3	25.1	16.2	6.5	4.5	2.4	5.8
Stock (200 - 299)	15.0	39.6	41.1	6.6	35.4	7.3	24.2
Quality (300 - 379)	13.6	23.8	21.6	4.6	32.4	9.3	7.3
Preferred (380 - 509)	7.5	7.8	8.0	6.2	27.6	22.2	15.5
Memorable (510 - 629)	1.5	1.6	0.0	0.6	1.3	3.6	3.6
Trophy ($630)	0.0	0.0	0.0	0.0	0.0	0.0	0.0

1d. Stock density indices.

Index	Keowee	Thurmond	Russell	Murray	Wateree	Marion	Moultrie
PSD	60	46	42	63	63	81	52
RSD-15	25	13	11	38	30	61	38
RSD-20	4	2	0	3	1	8	7

Recommendations

1. Show modeling results and demonstrate FAST software to management biologists.

2. Continue the compilation and evaluation of spring electrofishing data at Eastover.

3. Present findings to Wildlife and Freshwater Fishery Advisory Board.

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Appendix I

Population Dynamics and Management of Largemouth Bass in South Carolina

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Abstract

We employed a statewide standardized sampling plan and yield per recruit modeling to assess management alternatives for largemouth bass populations in South Carolina reservoirs. A protocol for conducting spring electrofishing was established. Reservoirs were divided into zones to account for spatial heterogeneity and sampled from 1997-99. Collected bass were measured and weighed. Reservoir-specific length-weight regressions were calculated. Otoliths were taken and sex was determined from a subsample of each 25 mm length group. Otolith aging was verified to ensure accuracy. Von Bertalanffy growth equations were developed for each reservoir using length at age information. From catch information, we estimated age-1 recruitment and total annual mortality. We then conducted yield per recruit modeling for five reservoirs which encompassed the range of growth and mortality conditions observed in South Carolina. We evaluated five minimum length limits ranging from 304 to 504 mm total length (TL) in 50 mm intervals. Modeling identified either 356 or 404 mm TL as the minimum length at which yield was maximized. In general, these minimum lengths resulted in harvest or catch and release fishery characteristics which met the objectives of management biologists.

Introduction

Largemouth bass is a sport fish of primary importance in South Carolina. Development of site-specific strategies that maintain strong reproductive potential and maximize harvest and catch of quality fish - as defined by anglers - is the state's overall management approach (South Carolina Department of Natural Resources 1995, unpublished). Kirk (1989) used a combination of creel survey, cove rotenone, and spring electrofishing to qualitatively determine the proper management strategy for large (>2000 ha) reservoirs in South Carolina. However, initial efforts to turn biological information into management actions met political resistance and failed. Currently, all small (< 200 ha) state-owned lakes have site-specific regulations while all large public reservoirs come under a statewide regulation of 10 bass per day with no size limit.

Sampling and management strategies needed to define and produce optimal fishing from a largemouth bass population have evolved substantially in the last half-century. Because of cost and logistic constraints, indices of abundance and population structure are the current basis of most management recommendations. Much of this approach stems from the pioneering work of Swingle (1950) in small ponds. Length-frequencies, length at age, and condition factors are basic indices used to describe a population's status at time of sampling. Calculation of proportional stock density (Anderson 1976) and relative weights (Wege and Anderson 1978) are indices that have been widely applied by management biologists.

From a sampling viewpoint, electrofishing has become the primary tool as catches reflect population structure and abundance (Weithman et al. 1979; Hall 1986; McInerny and Degan 1993). Electrofishing sampling strategies must now consider location (Siler et al. 1986) and habitats (Sammons and Bettolli 1999) within a reservoir as these variables can influence bass abundance. Otoliths are generally preferred to scales when obtaining estimates of age. In South

Carolina, Morrow (1990) demonstrated that otoliths provided more precise estimates than scales. A survey of natural resource agencies in the southeastern United States indicated that most states were moving toward standardization of black bass management tools, with the development and implementation of management plans, sampling plans, and population assessment guidelines (Bulak et al. 1998).

Mathematical modeling of population structure under various management scenarios is a tool that will become more popular as our ability to process information increases. Ricker (1958) showed that population structure and abundance vary according to three rate functions - recruitment, growth, and mortality. In his later classic text, Ricker (1975) compiled various mathematical solutions to compute and interpret the biological statistics of fish populations. Managers have long-realized the value of having good estimates of growth, mortality, and recruitment, but have acknowledged that getting them can be expensive and difficult and, perhaps, not worth the effort (Novinger 1984). However, in recent years managers have begun to use models as tools. For example, Zaggar and Orth (1986), used computer simulations to evaluate the management implications of different largemouth bass harvest regulations. Obtaining rate estimates from historical studies on 698 bass populations, Beamesderfer and North (1995) used yield per recruit modeling to evaluate population response to regulations at differing levels of growth and natural mortality.

The primary objective of this project was to refine efforts to use a standardized sampling approach to define optimal site-specific management strategies. Within this overall objective, we desired to: 1) employ standardized spring electrofishing to obtain estimates of population structure and abundance, growth, mortality, and recruitment; 2) develop a statewide database; and 3) use estimates of growth and mortality in a yield per recruit model to initially evaluate statewide management options.

Methods

Beginning in 1997 largemouth bass populations in South Carolina reservoirs were sampled by electrofishing during spring in accordance with a standardized sampling plan (SSP) developed by the South Carolina Department of Natural Resources (SCDNR) (Bulak et al. 1998). Under the plan, large reservoirs (>2000 ha) were divided into three or more zones depending on their spatial complexity. Each zone was divided into sample sites, defined as shoreline areas that would support 30 minutes of electrofishing without overlap. Three primary sample sites were selected at random in each zone. Secondary sites were chosen in the event that target numbers of fish were not captured at the primary sites. Effort was recorded as seconds of electrofisher-on time, summed across sampling sites for each zone.

The sampling objective was to collect 30 fish per sample site and 80 fish per zone. Measurements included total length (TL) in mm and weight in g. For each reservoir, the $\log_{10}$ transformed length-weight regression was calculated from 1997-99 data for all bass greater than or equal to 254 mm TL. Catch per unit effort (CPUE) was calculated as an estimator of abundance. When age and sex information were needed, up to four fish per 25-mm length group were collected per zone toward a target of 10 fish per 25-mm length group per reservoir. Fish collected for age and sex information were sacrificed to remove otoliths and inspect gonads. Fish <175 mm TL were assumed to be age-1, and were generally released. The SSP required field biologists to take otoliths from fish <475 mm TL in 1997 and <575 mm TL in 1998 and 1999; some samples were intermittently collected from larger fish. The SSP recommended that age data be collected from reservoirs for three consecutive years to provide a measure of annual variation in recruitment, growth, and mortality.

Otoliths were processed by field biologists, and were aged whole or in transverse section, using standard techniques. Sub-sets of otoliths from each reservoir were sent to the SCDNR Freshwater Fisheries Research lab in Eastover for verification and standardization of age interpretation. If the level of agreement between the field and Eastover was less than 90%, otoliths were read jointly to discover if differences were random or systematic. If agreement on age interpretation couldn’t be reached, those fish were omitted from analyses involving age. Collection data were also sent to Eastover for analysis and incorporation into a statewide database.

Population age structure was determined from age-length keys prepared from fixed length-group subsamples (DeVries and Frie 1996). A multi-year composite age-length key constructed from merged annual data was used for each reservoir. Age-frequency distributions were computed by applying the age-length key to the population’s length-frequency distribution. If the upper length limit of fish aged caused the length-frequency distribution for an age class to be truncated, estimates of population parameters (mean length-at-age and number of fish per age class) derived for that and higher age classes were considered biased.

Growth was initially computed from length-at-age data derived from age-frequency distributions. However, growth estimates were not realistic because of the absence of unbiased data from older, longer fish. Supplemental length-at-age data for three reservoirs (Murray, Wateree, and Santee-Cooper) were obtained from a genetics study of trophy bass conducted between 1993 and 1997. Cooperating taxidermists removed otoliths and recorded total lengths of largemouth bass submitted to them by anglers (Bulak et al. 1998). Estimates of maximum total length and maximum age for largemouth bass in each of the study reservoirs were obtained by reviewing available sampling records, from the present as well as other recent population studies.

Predicted length at age of largemouth bass in each study reservoir was estimated by solving the von Bertalanffy growth equation (Ricker 1975):

(1) $L_t = L_4(1-e^{-k(t-to)})$

where L_t = total length at time t,

L_4 = maximum theoretical length,

t = time or age in years,

t_0 = time in years when length = zero.

For ages 1 through 5, the unbiased mean length at age was used. For ages 6 and above, we used age at length data from either a trophy largemouth bass database or best available length at age estimates from otolith aging conducted on 1997-99 samples. Where appropriate, the longest non-aged bass from a reservoir was assigned an age of 14. The equation was solved with Fishery Analyses and Simulation Tools (FAST) software (Slipke and Maceina 2000).

CPUE was calculated by age class for each reservoir. The number of fish per age class derived from age-frequency tables was divided by the total effort expended, expressed in hours. CPUE of age-1 largemouth bass was used as an index of recruitment. Differences in age-1 CPUE between years provided a measure of the inherent variability of recruitment within each reservoir. Mortality rates were also calculated using CPUE.

To define mortality, we used the equations of Ricker (1975) for a Type II fishery, in which natural and fishing mortality act concurrently. The equations were:

2) $Z = F + M$,

3) $A = 1 - e^{-Z} = u + v = m + n - mn$,

4) $n = 1 - e^{-M}$,

(5) $m = 1 - e^{-F}$,

where Z = instantaneous total mortality rate,

F = instantaneous fishing mortality rate,

M = instantaneous natural mortality rate,

A = annual total mortality (%),

u = annual exploitation (%),

v = annual natural mortality (%),

n = conditional natural mortality expected in the absence of fishing mortality (%),

m = conditional fishing mortality expected in the absence of natural mortality (%).

Estimates of annual total mortality were derived from spring electrofishing catch curves (Ricker 1975). Depending on the data available, we estimated annual mortality from both aggregate and cohort-specific catch curves. Up to three equations that best fit the data were identified and, based on descriptive statistics and professional judgment, an overall best estimate of total annual mortality in each reservoir was defined. Age-classes that were not effectively sampled were not included in the analysis.

Stock density indices (PSD, RSD-P, and RSD-M) were computed annually for each reservoir using the traditional method of Gablehouse (1984). Minimum stock length, preferred (P), and memorable (M) bass were defined as 20, 38, and 51 cm TL respectively, as described by Anderson and Neumann (1996). Multi-year means were calculated for each index to categorize population balance.

To broadly evaluate the minimum size limit that would maximize yield if instantaneous harvest were possible, we constructed a simple model to estimate the critical age (Ricker 1975) of the fastest and slowest growing populations. Simulations were initialized with 1,000 age-1 recruits and conducted at conditional natural mortalities of 0.15 and 0.27. Length and weight at age were defined by reservoir-specific length-weight regressions and von Bertalanffy growth equations. Cohort biomass was calculated at 0.5 year intervals.

Yield per recruit analysis in FAST was used to evaluate bass fisheries in five reservoirs. FAST computed yield (Y, in weight) with the Jones modification of the Beverton-Holt equilibrium yield equation found in Ricker (1975, equation 10.22). The equation was further modified to:

$$(6) \qquad Y = \frac{FN_t e^{(Zr)} W_\infty}{K} \left[\beta\left(X, P, Q\right)\right] - \left[\beta\left(X_1, P, Q\right)\right]$$

where F = instantaneous rate of fishing mortality,

N_t = number of recruits entering the fishery at some minimum length at time $_t$,

Z = instantaneous rate of total mortality,

r = time in years to recruit to the fishery,

W_4= maximum theoretical weight,

K = von Bertalanffy growth coefficient,

$ = incomplete beta function,

$X = e^{-Kr}$,

$X_1 = e^{-K(\text{Max age - to})}$,

P = Z/K, and

Q = slope of weight-length relation + 1.

Equation (6) computed yield where recruitment, growth, length-weight relationship, conditional natural mortality, and conditional fishing mortality were constant for each simulation. Length when fish enter the fishery was the primary variable evaluated. Full details of the equation are provided in Slipke and Maceina (2000).

Prior to running the simulations, we asked management biologists to identify their objectives for the five study reservoirs. After the simulations were run, a minimum length limit that maximized yield under existing mortality conditions was identified. We then evaluated how well the minimum length limit met identified management objectives.

Results

Nine large reservoirs were sampled using the SSP between 1997 and 1999, though not all were sampled each year. In 1997 five large reservoirs were sampled: Thurmond, Secession, Greenwood, Marion, and Moultrie. In 1998 Russell, Murray, and Wateree were added. In 1999 Keowee was added while Greenwood was dropped. Marion and Moultrie were sampled independently, but results were combined and reported as Santee-Cooper, since the two reservoirs are considered to be a single management unit.

Abundance of largemouth bass varied by year and reservoir (Table 1) . Total CPUE ranged from 24.4 fish per hour in Murray (1999) to 101.2 fish per hour in Wateree (1999). Fish five years old or younger accounted for more than 90% of the total CPUE in most of the reservoirs. The Santee-Cooper population was old, by contrast; younger fish were generally less than 80% of the total CPUE in the this lake system.

Age-1 CPUE varied annually, within and between reservoirs (Table 1). Catch of age-1 largemouth bass ranged from 3.6 fish per hour in Lake Moultrie in 1997 to 39.8 fish per hour in Lake Thurmond in 1999. Average recruitment was highest in Lake Thurmond (26.2 fish per hour) and lowest in Lake Murray (9.0 fish per hour), among reservoirs with multiple years of sampling (Table 1).

Annual total mortality rate ranged from 25 to 52.5% in seven major reservoir systems

(Table 2). For each reservoir, three independent estimates of total mortality generally agreed with each other, increasing confidence in the final estimate.

Mean lengths-at-age computed from age-frequency distributions were unbiased through age 5 in all reservoirs except Murray and Greenwood, which were unbiased through age 4. Differences in growth rates between reservoirs were apparent (Table 3). The Santee-Cooper population grew fastest, averaging more than 5 cm longer than Russell fish at age 5. Older bass captured by electrofishing were considerably smaller at age than trophy fish captured by anglers (Table 3).

Von Bertalanffy-predicted length at age varied among reservoirs and differences tended to increase with age (Table 4). The Santee-Cooper population was the fastest growing, taking 4.09 years to reach 406 mm TL. The Keowee population was the slowest growing, taking 4.77 years to reach 406 mm TL. Growth rates in Thurmond and Murray were intermediate and very similar to each other. The Wateree population exhibited intermediate growth at age 4 but was approaching slow growth at age 10.

Relative plumpness of largemouth bass populations, estimated from length-weight regressions, varied among reservoirs (Table 5). In general, differences in relative plumpness increased as length increased. Also, faster growth within a reservoir corresponded to increased plumpness.

Stock density indices indicated that South Carolina’s major reservoirs were structurally diverse in terms of their largemouth bass populations. Though stock density indices for Santee-Cooper’s bass population declined steadily during three years, the population met the criteria for management under the “big bass” option established by Willis et al. (1993): PSD 50-80, RSD-P 30-60, and RSD-M 10-25 (Table 6). All of the other bass populations were clearly “balanced”

(PSD 40-70, RSD-P 10-40, RSD-M 0-10) except Lake Russell's, which bordered on the "panfish" category (PSD 20-40, RSD-P 0-10) (Table 6).

Critical age determination demonstrated the effects of rate of growth and natural mortality on harvest potential of bass populations in South Carolina reservoirs (Figure 1). At natural mortalities of 0.15 and 0.27, the relatively fast-growing Santee-Cooper population reached maximum biomass at ages 8 and 5 respectively, while the Keowee population reached maximum biomass at ages 6.5 and 4.5, respectively. However, at similar rates of natural mortality, the simulated Santee-Cooper cohort produced at least twice as much biomass as the Keowee cohort.

Yield per recruit modeling - Parameter selection

Reservoir-specific estimates of the length-weight relationship and growth were used in simulations. Based on aging results, we defined 14 years as the maximum age of largemouth bass in all South Carolina reservoirs.

There were no estimates of natural mortality of largemouth bass in South Carolina. However, Allen et al. (1998) listed 10 estimates of natural mortality, ranging from 21 to 78% with a median of 33%, in Type II fisheries in Georgia, Alabama, and Tennessee. Combining these estimates with professional judgment, we defined high (30%), moderate (22.5%) and low (15%) levels of natural mortality that would be expected in South Carolina. These values were used in yield per recruit simulations.

Using catch curve results, where total annual mortality ranged from 25 to 52.5%, and natural mortality estimates, we defined conditional fishing mortality in all reservoirs as ranging from 0.10 to 0.35 in 0.05 intervals, allowing us to simulate a range of possible conditions for each reservoir. In simulations, low, moderate, and high exploitation (u) was defined as #0.15, between 0.15 and 0.30, and $0.30, respectively.

Based on the levels of exploitation and natural mortality generated in simulation runs, we identified nine simulations that had each possible combination of low, moderate, and high levels of natural and fishing mortality. Minimum total lengths of 304, 354, 404, 454, and 504 mm were evaluated in these nine simulations for each reservoir.

Yield per recruit modeling - Simulation output

Under current mortality conditions in each reservoir, either a 354 or 404 mm minimum length limit maximized yield (Table 7). The minimum length limit that maximized yield was a function of growth and mortality rates. At the highest level of natural mortality (v $ 0.255), the 304 mm minimum length limit maximized yield for all five reservoirs. As natural mortality decreased and fishing mortality increased, increasingly higher minimum length limits maximized yield. The maximum yield of 626 kg was produced in the fast-growing Santee-Cooper population under low natural and high fishing mortality conditions. Under identical conditions, the relatively slow-growing Lake Keowee population produced 395 kg.

Identifying the minimum size limit that would maximize harvest did a reasonable job of satisfying management objectives stated for each reservoir. A brief review of each reservoir using results from the nine simulations follows.

The stated management objective for Santee-Cooper was to maximize harvest of 457 mm fish (0.25 weighting) and maximize CPUE of 559 mm fish by catch and release anglers (0.75 weighting). The relatively high growth rate, RSD-M of 11, and low total annual mortality (below 0.30) suggest that Santee-Cooper can be managed for trophy bass. Simulations indicated maximum harvest would be obtained with a 404 mm size limit and the average size of the harvested fish would weigh 1909 g, which corresponds to a 509 mm bass.

On Lake Murray, the manager wished to maximize the harvest of 381 mm bass. The low natural and fishing mortality simulation suggested a 404 mm minimum size limit would maximize harvest and an average harvested fish would measure 495 mm. A 304 minimum size limit resulted in a 5% decline in total yield, a 39% increase in number harvested, and a 439 mm TL average size.

The growth rate of Lake Thurmond bass was similar to those from Lake Murray, but the estimated total annual mortality (0.525) was much higher. Since Bettross et al. (1994) had estimated exploitation of about 0.35 on Lake Thurmond, we concluded that natural mortality was moderate (i.e. <0.25). Thus, simulations suggested a minimum size limit of 404 mm would maximize biomass harvest (0.5 weighting) and achieve a mean size at harvest of 457 mm.

In Lake Wateree, the manager's goal was to achieve an average harvest size of 406 mm. Simulations suggested that a minimum size limit of 354 mm would maximize harvest with an average fish measuring 422 mm.

Lake Keowee had the slowest growing population of those evaluated. The manager desired to maximize harvest (0.4 weighting) and CPUE (0.6 weighting) of 457 mm bass. Assuming a moderate amount of natural mortality in Lake Keowee, simulations suggested that a 354 mm minimum size limit would maximize harvest, with an average bass measuring 415 mm. If a 404 mm size limit was implemented, simulations indicated yield would be decreased by 6% and numerical harvest by 26%, but mean length at harvest would increase to 448 mm. Relatedly, if we had assumed that natural mortality was low in Lake Keowee, a 404 mm minimum size limit would have maximized yield and produced bass that averaged 450 mm TL.

Discussion

Three years of standardized sampling on South Carolina's major reservoirs yielded estimates of growth, mortality, and recruitment. These estimates were adequate to initially assess management strategies in a yield per recruit simulation model. Simulation output indicated statewide consideration of either a 356 or 404 mm length limit would improve the quality of fishing. Standardized sampling and subsequent modeling identified that additional sampling was needed to verify the accuracy of rate functions used in population assessments.

When constructing a database, the accuracy of otolith aging should not be taken for granted. Initial age estimates received from field biologists did not, in some cases, agree with our estimates. Re-inspection of spring-caught samples indicated a new annulus was just forming, causing some misinterpretations. It was important to have a protocol in place that verified age interpretation.

Estimated growth rates observed in South Carolina were higher than average for the United States (Carlander 1977) and comparable to growth rates observed in Florida (Porak et al. 1986) and Texas (Siedensticker 1994). A biased sampling strategy and possible gear selectivity affected our ability to estimate length at age for bass age-5 and older. Our sampling strategy, which set an upper length limit for otolith collections, selected for slower growing individuals of older cohorts. This strategy was implemented at least in part because some field biologists had public relation concerns regarding the sacrifice of larger bass. We have now modified our Standardized Sampling Plan by eliminating the upper length limit for otolith collections. It is worthwhile to sacrifice a few fish to obtain good estimates of the growth rate of older bass, which are highly coveted by anglers. Our growth estimates also showed a tendency for inter-reservoir growth differences to increase in the older age classes, further supporting full sampling of older age classes. Growth estimates from taxidermist-supplied otoliths were substantially higher than estimates obtained from electrofishing, a phenomenon also observed by Crawford et al. (1996) in Florida. This suggested that one or both collection methods have inherent bias. However, access to taxidermist-supplied trophy specimens allowed us to more reliably estimate the growth rate of older age classes and determine bass longevity in South Carolina.

While catch curve analysis provided good initial estimates of total bass mortality, future efforts need to better define the rates of fishing and natural mortality. Estimates of natural mortality for largemouth bass vary widely. Carlander (1977) and Allen (1998) report natural mortality estimates in the literature of 0.01 to 0.57 and 0 to 0.78, respectively. Using the mean annual temperature equation supplied by Beamesderfer and North (1995), we calculated an expected range of instantaneous natural mortality (M) in South Carolina of 0.55 to 0.63, or annual natural mortality (v) of 0.42 to 0.47. Intuitively, these estimates appeared high to us as otolith aging confirmed that age-10 bass are relatively common and bass in South Carolina can live to age-14. An M of 0.6 over 10 years would lead to a 0.2 percent survival. Field evaluations of either exploitation or natural mortality in un-fished systems are needed to better define the relative importance of each mortality component. From a regulatory point of view, modeling suggested that if the annual natural mortality rate was 0.30 or greater, maximum sustained yield would be obtained with a 304 mm size limit and trophy management options would be limited.

Variable recruitment was not considered in population simulations, even though it could have been easily evaluated using FAST. However, Beamesderfer and North (1995) compared the results of constant and variable recruitment simulations and found no substantial differences. From a management perspective, we agree with Beamesderfer and North (1995) that constant recruitment simulations accurately estimate the average response of a fishery and that results obtained from them are applicable unless regulations are changed from year to year according to year-class strength. In future years, when additional data are available and base management recommendations have been implemented, it will become more appropriate to consider the effects of variable recruitment on regulations. Relatedly, simulation results were based on constant rates of fishing and natural mortality. We recognize that mortality rates may change or be dependent on population structure; continued monitoring should allow us to adjust these rates as needed.

Why did we expect that yield per recruit modeling would provide reasonable guidelines to largemouth bass fisheries that may have a high percentage of catch and release anglers? As our survey of management biologists demonstrated, there is a general desire to provide both harvest and catch and release anglers with quality fishing. Yield per recruit modeling identified the point where population growth, a function of lake productivity, and abundance have combined to maximize biomass harvest under existing mortality conditions. Thus, managers can use yield per recruit results as a guidepost to identifying the scenario that produces the greatest abundance of "quality" fish. As management goals or the characteristics of the fishery change, managers can run additional simulations that will possibly identify new guideposts.

We did not consider slot limits at this time, though FAST was capable of performing these assessments. Protective slot limits are generally useful when high recruitment causes a density-dependent growth suppression (Anderson 1976 , Dean and Wright 1992), though concern exists that anglers often will not harvest bass below the protected slot size (Martin 1995). When sufficient data becomes available, we will assess whether growth is affected by recruitment in any of our impoundments. If density-dependent growth suppression is exhibited and managers are confident that harvest below the slot will occur, we will evaluate slot limits.

Population modeling provides a dynamic environment for assessing population responses to key rate parameters, such as growth and mortality. As with any model, output is only as good as the quality of input data. In our case, we incorporated best-available estimates of input to get an initial idea of management strategies that are needed in South Carolina. The process has identified areas where improved estimates are needed. As estimates change or as we wish to assess a theoretical change in a parameter, we now have a mechanism to project what these changes will mean to the population. Commitment to this approach in the future will lead to reservoir-specific models able to reliably predict population responses. Potentially, public demonstration of this approach can be used to further inform and educate anglers.

For South Carolina, the decision-making process will need to change if we are to use best-available science to maximize the efficiency and responsiveness of largemouth bass management. Our survey of the southeastern states recognized that South Carolina is the only state where management recommendations must receive Legislative approval. At present, this process has inhibited the ability of management to quickly react to population dynamics and angler needs.

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Table 1. Electrofishing CPUE of largemouth bass by reservoir during 1997-1999 using a standardized sampling protocol. Values are included for age classes which were not truncated, and therefore biased, by the upper size limit of fish sacrificed for otolith aging.

		Reservoir								
Year	Age	Keowee	Thurmond	Secession	Russell	Greenwood	Murray	Wateree	Marion	Moultrie
1997	1		21.8	8.7		27.0			10.6	3.6
	2		25.3	21.0		12.8			6.5	6.9
	3		9.0	13.8		6.3			8.2	8.6
	4		4.9	4.3		2.8			5.8	7.1
	5		2.6	3.6					4.3	6.0
	Total		64.8	56.1		53.0			49.0	50.3
1998	1		16.9	5.3	13.1	11.1	7.2	10.6	20.2	10.7
	2		18.9	10.5	13.6	15.5	6.7	22.3	7.0	5.9
	3		6.4	12.0	3.8	7.1	2.9	18.8	5.7	7.3
	4		3.5	1.8	2.2	3.3	3.2	7.4	5.5	5.8
	5		2.5	5.8	0.9			4.7	4.7	6.1
	Total		50.0	38.8	33.8	43.6	26.9	73.4	57.8	50.0
1999	1	13.7	39.8	17.0	20.9		10.8	11.7	7.8	26.7
	2	13.2	35.3	20.5	41.1		4.7	42.7	7.8	6.9
	3	7.4	11.6	15.5	12.4		1.9	24.2	6.9	5.0
	4	2.9	5.6	6.5	5.8		2.3	7.6	5.8	3.8
	5	2.6	2.9	6.0	3.6			5.4	3.6	4.2
	Total	43.9	97.8	71.5	86.9		24.4	101.2	44.9	56.4

Table 2. Estimated total annual mortality (A) from seven South Carolina reservoirs; the final estimate of A is based on the preceding estimates and best professional judgment. Estimates denoted with ***, **, and * were significant at P = 0.01, 0.05, and 0.10, respectively. Years marked with ^{c} identify cohort-specific catch curves while all others are aggregate catch curves from all sampling years.

Reservoir	First estimate			Second estimate			Third estimate			Final estimate
	A (%)	Year(s)	Ages	A (%)	Year(s)	Ages	A (%)	Year(s)	Ages	A (%)
Thurmond	52.5***	1997-99	2-5	56.6***	1997-99	2-4	53.3	1995^{c}	2-4	52.5
Santee-Cooper	22.4***	1997-99	1-5	17.4*	1997-99	2-5	40.0*	1994^{c}	3-5	25
Secession	54.2***	1997-99	2-4	37.4***	1997-99	2-5	50.8*	1995^{c}	2-4	47.5
Greenwood	43.2***	1997-98	1-5	47.0***	1997-98	2-5	54.6***	1997-98	2-4	47.5
Murray	29.5***	1998-99	1-5	24.3*	1998-99	2-5	37.1	1998-99	2-4	30
Wateree	47.7***	1998-99	2-5	51.4***	1998-99	3-5	50.7**	1998-99	2-4	50
Keowee	44.1**	1999	2-5	38.4**	1999	1-5	53.1	1999	2-4	45

Table 3. Mean lengths (cm) of otolith-aged largemouth bass in South Carolina reservoirs, from two sources. Fish were collected by electrofishing (E) during spring, 1997-1999, and from taxidermists (T) mounting trophy fish from three reservoirs in 1993 and 1997. Fish collected by electrofishing were subsampled for aging. Mean lengths of those fish reported in **bold** were computed from unbiased age-frequency distributions; those in plain text were computed for older fish, and were biased because fish longer than 57 cm (47 cm in 1997) were not routinely included in the subsampling procedure. TL of the largest fish recorded for each reservoir is included.

		Age													Largest
Reservoir	Source	1	2	3	4	5	6	7	8	9	10	11	12	13	(14)
Santee-Cooper	E	**19.1**	**32.7**	**37.9**	**41.1**	**44.5**	45.5	46.2	48.8	48.0	52.1	50.0	54.2		69.8
	T					60.6	60.3	62.1	63.9	64.8	65.6	65.7	66.0	65.4	
Murray	E	**18.4**	**30.0**	**36.0**	**39.4**	43.0	44.0	43.8	45.0		40.8				66.0
	T						54.2	53.5	57.5	61.0	58.9	57.2	59.1		
Wateree	E	**19.1**	**28.4**	**36.0**	**40.0**	**43.0**	44.7	46.4	45.8	50.4	49.4	50.4			58.1
	T				47.1	48.6	49.3	49.8		54.2		50.8		54.5	
Thurmond	E	**17.9**	**28.5**	**34.8**	**38.9**	**43.7**	44.8	47.4	47.0		49.3	50.0			61.5
Secession	E	**16.9**	**28.4**	**34.3**	**38.9**	**42.2**	43.7	46.9	47.8	45.7		43.8			61.3
Russell	E	**17.2**	**27.4**	**33.2**	**35.0**	**39.2**	43.7	48.7	42.4			47.3			52.2
Greenwood	E	**16.8**	**29.2**	**35.6**	**40.9**	42.2	47.2	47.1	44.3		54.9				61.5
Keowee	E	**18.0**	**27.9**	**34.8**	**38.3**	**41.8**	43.8	47.9	44.5	48.9	43.4	53.4	51.2		55.9

Table 4. Von Bertalanffy growth equation parameters and predicted length at age for largemouth bass in five reservoirs in South Carolina. All equations were significant at P#0.01.

				Predicted length (mm) at age (years)		
Reservoir	L4	K	t_0	4	7	10
Santee-Cooper	782	0.124	-1.812	402	520	602
Wateree	565	0.255	-0.705	395	486	528
Murray	730	0.131	-1.648	381	494	571
Thurmond	696	0.153	-1.191	381	497	570
Keowee	563	0.226	-0.890	377	468	515

Table 5. Log$_{10}$ transformed length-weight regressions and calculated weight (g) at total length (mm) for five South Carolina reservoirs. Data was collected in the period 1997-99. All regressions were significant at P#0.01.

					Calculated weight at length		
Reservoir	N	R^2	intercept	slope	305	406	508
Thurmond	655	0.98	-5.73	3.32	326	851	1791
Santee-Cooper	1195	0.98	-5.43	3.22	363	921	1895
Murray	240	0.98	-5.17	3.11	367	904	1817
Wateree	674	0.98	-5.65	3.32	378	988	2077
Keowee	457	0.92	-5.23	3.13	344	849	1712

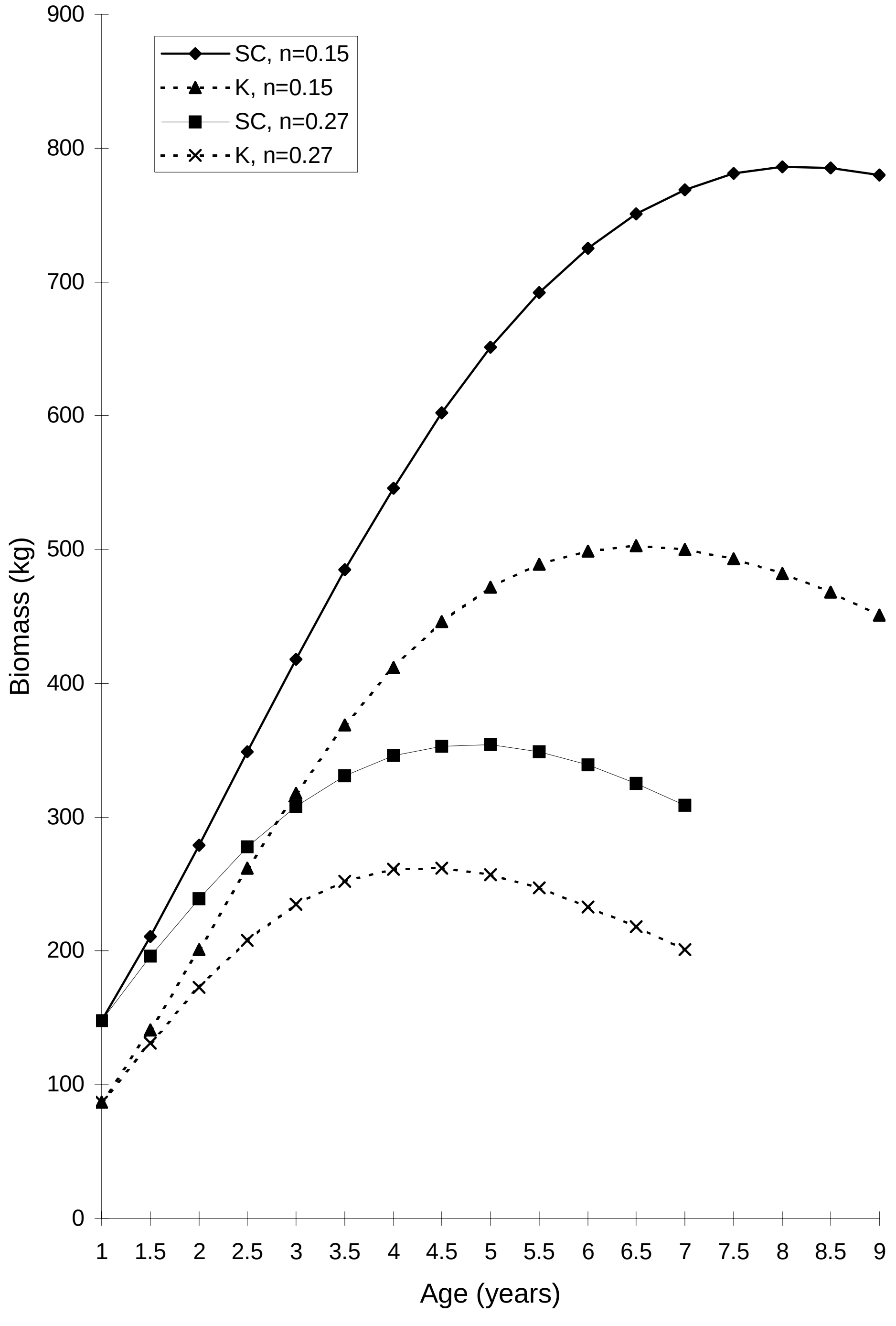
Table 6. Stock density indices of selected South Carolina reservoirs, by year, with means. Minimum stock length, preferred (P), and memorable (M) bass were defined as 20, 38, and 51 cm TL, respectively.

Reservoir	Year	PSD	RSD-P	RSD-M
Santee-Cooper	1997	93	70	14
	1998	86	64	12
	1999	65	47	8
	0	81.3	60.3	11.3
Murray	1998	75	45	4
	1999	63	37	3
	0	69.0	41.0	3.5
Secession	1997	61	23	5
	1998	75	34	3
	1999	63	28	1
	0	66.3	28.3	3.0
Wateree	1998	69	39	1
	1999	63	29	1
	0	66.0	34.0	1.0
Keowee	1998	68	31	3
	1999	60	25	4
	0	64.0	28.0	3.4
Greenwood	1997	51	20	2
	1998	67	28	4
	0	59.0	24.0	3.0
Thurmond	1997	49	15	0
	1998	56	20	1
	1999	45	12	2
	0	50.0	15.7	1.0
Russell	1998	45	7	0
	1999	41	11	0
	0	43.0	9.0	0

Table 7. For varying levels of mortality, the minimum length limit (Len) that will produce maximum yield of largemouth bass in five South Carolina reservoirs. The mean weight (W̄t) of a harvested bass at each length limit is also identified. Mortalities that most closely resemble observed conditions in each reservoir are underlined.

			Reservoir														
Mortality			Santee-Cooper			Keowee			Thurmond			Murray			Wateree		
v	u	A	Len	Yield	W̄t	Len	Yield	W̄t	Len	Yield	W̄t	Len	Yield	W̄t	Len	Yield	W̄t
.139	.139	.278	404	494	1909	354	309	1094	404	390	1654	404	405	1680	354	413	1383
.131	.232	.363	454	585	2130	404	368	1237	454	475	1880	454	478	1907	404	495	1539
.123	.325	.448	504	626	2490	404	395	1170	454	507	1769	454	512	1798	404	527	1442
.214	.088	.303	304	207	1226	304	135	887	304	164	1076	304	171	1091	304	182	1124
.203	.177	.380	354	282	1315	304	192	785	354	226	1167	354	234	1193	354	256	1226
.191	.267	.458	404	315	1518	354	217	909	404	253	1361	354	262	1067	354	292	1120
.286	.084	.370	304	110	1044	304	73	798	304	85	928	304	90	947	304	100	1001
.271	.169	.440	304	160	896	304	111	718	304	124	804	304	133	827	304	150	892
.255	.255	.510	304	181	784	304	132	653	304	142	708	304	153	734	304	175	802

Figure 1. Critical age determination at two conditional natural mortalities (n) for fast-growing Santee-Cooper (SC) and slow-growing Keowee (K) largemouth bass populations in South Carolina.



JOB PROGRESS REPORT

STATE: South Carolina PROJECT NUMBER: Broad River

PROJECT TITLE: Fisheries Investigations in Lakes and Streams - Statewide

STUDY: Research

JOB TITLE: An Inventory of the Aquatic Resources of the Broad River, with Emphasis on Fishes.

Introduction

The Broad River Trust Fund was established with monies provided by the power companies that own and operate hydroelectric dams on the Broad River, in partial mitigation for fish killed by the operation of those dams. The Trust Fund resulted from an agreement negotiated between SCDNR, USFWS, Duke Power Company, and South Carolina Electric & Gas Company, as a result of the FERC relicensing process. Trust Fund monies are administered by a board of trustees composed of representatives of each of the entities involved. The monies are intended to be used to enhance the fishery resources of the Broad River. The trustees decided that before any enhancement activity took place, a preliminary survey of the fish community was needed to determine its status and condition. The present study was undertaken to provide that information.

Methods and Materials

Preliminary reconnaissance of the Broad River was conducted by john boat during low water conditions in Spring, 2000, to collect habitat information and identify potential sample sites. Information derived from the survey was compiled in a geographic database using ArcView GIS software. Other sources of geographic data were obtained and incorporated into the database. A study plan was developed and submitted to the trustees for comment and approval (see

Appendix I).

We limited the collection of habitat information to riverine areas in the Broad River. Riverine areas were defined as portions of the Broad River least impacted by reservoir ponding. The Broad River was traversed in a john boat during low water conditions. Macro-habitat along the course of the river was classified into one of five groups (Table 1). The upstream and downstream limit of each habitat unit was recorded with a Trimble GPS unit. GPS locations were differentially corrected using Pathfinder Office software and transferred into the geographic database using ArcView GIS software. The GPS locations were then used to divide the Broad River into the appropriate habitat units.

Results and Discussion

Several layers of information were included in the Broad River geographic database comprising access areas, historic fish sampling sites, water quality sampling sites, NPDES discharge sites, riparian land cover, USGS gages, and a habitat map. We surveyed the river for suitable access points and recorded their position with the GPS unit. Duke Power and SCE&G provided us with reports from their past fishery surveys. Water quality sites monitored by DEHC and NPDES discharge sites were obtained from DEHC. Riparian land cover was downloaded from the SCDNR web page. Point locations for USGS gages were digitized from topographic maps. Finally, we incorporated the results from our habitat inventory into the database.

We completed habitat mapping on 53 km of the Broad River encompassing a total area of 531 ha. Thirty-seven km remain to be inventoried. Pools were the most common habitat type and accounted for 52% of the total area inventoried (Table 2). Glide habitat was abundant and accounted for 25% if the total area inventoried. Nineteen percent of the area inventoried was shoal habitat. Run habitat contributed 3% and riffle habitat was the least common contributing only 1% to the total area inventoried.

Recommendation

Continue study as planned, conducting fish population sampling in Fall, 2000 and Spring, 2000.

Table 1. Habitat unit definitions for visual assessment.

Habitat Type	Description
Riffle	Relatively shallow (<0.5m), swift flowing section of river where water surface is broken.
Glide	Relatively shallow (<1m); with visible flow but mostly laminar in nature; minimal observable turbulence; relatively featureless bottom.
Run	Deep (>1m), swift flowing sections with turbulent flow; surface generally not broken.
Pool	Deep (>1m) slow moving sections.
Shoals	Shoal area; which may contain a variety of habitat complexes.

Table 2. Results of the habitat inventory of the Broad River.

Habitat Type	Number of Units	Mean Area (ha)	Total Area (ha)
Pool	46	5.9	276
Glide	43	3.1	134
Shoal	40	2.5	100
Run	8	1.8	15
Riffle	3	1.8	6

Prepared by: Jason Bettinger Title: Fishery Biologist

Appendix

An inventory of the aquatic resources of the Broad River, with emphasis on fishes.

Introduction

Baseline information on the present status and composition of the aquatic community of the Broad River watershed is needed to develop effective management and enhancement plans. The fishery resources of the Broad River watershed have received little attention; the composition and status of the community are not comprehensively defined. In response to federal relicensing activity in the last decade, spot surveys of the fish community were conducted in the immediate vicinity of hydropower dams; little sampling has occurred in reaches of the river between these dams.

A comprehensive inventory is the first piece of information needed to develop effective natural resource management plans and identify fish enhancement opportunities for the Broad River. This survey will characterize the composition and biotic health of the fish community at sampled habitats along the entire river, establishing, for the first time, a baseline condition of the fish community in the Broad River. The relative condition of the fish community can serve as a general indicator of the health of the aquatic community in a river reach (Karr et al., 1986).

Use of a geographic database will define physical and chemical features of the basin that can affect the condition of the fish and aquatic community. Substantial amounts of information have been gathered on hydrology, geology, and water quality. This study will add information on the condition of riparian buffers, outfalls, and tributaries. Information obtained will be added to the existing database on hydrology, geology, and water quality and correlated with biotic information gathered in the study.

Objectives:

1) To comprehensively inventory the aquatic resources of the Broad River watershed, with emphasis on fishes.
2) To compare the fish community along the length of the river, examining the possibility of fish community fragmentation associated with dams.
3) To compile habitat and natural resource data obtained in the current study and in previous efforts on a watershed-based database and investigate relationships between the status of the fish community and environmental variables such as dam location, hydrology, water quality and quantity, and adjacent land-use.
4) To use the data collected from this effort to identify opportunities for protecting and enhancing the aquatic resources of the Broad River, with emphasis on the fish community.

Study Area

The Broad River basin originates in North Carolina and dominates the central Piedmont of South Carolina. Within South Carolina, the river flows approximately 100 miles until it merges with the Saluda River to form the Congaree River. Excluding the Enoree River, the Pacolet River and the Tyger River Basins the Broad River Basin includes 1,845 square miles. Most of the basin is forested (72%); the remainder of the land is largely agricultural (12%) and urban (8%) (SCLRCC 1990). Average flow of the Broad River approximately 7 miles downstream from the North Carolina line (USGS gage # 1515) was 2,470 cfs while average flow 10 miles below Parr Reservoir (USGS gage #1615) was 6,250 cfs. In the upper part of the basin, where annual rainfall is highest, flows are well-sustained and moderately variable; downstream, flows become more variable as rainfall and groundwater support decreases (Snyder et al. 1983). Seven hydropower dams are located on the South Carolina portion of the Broad River; these are Gaston Shoals, Cherokee Falls, Ninety-Nine Islands, Lockhart, Neal Shoals, Parr Shoals, and Columbia. Climatological, hydrological, and limnological changes along the River's course create a variety of habitat types for aquatic organisms residing in the Broad River.

The S.C. Department of Health and Environmental Control recently characterized water quality and the associated status of the aquatic community at nine assessment sites in the Broad River (DHEC 1998). At several sites aquatic community health and/or recreational uses were compromised by excessive levels of chemical or bacterial contamination. The aquatic community was not fully supported in the Broad River at SC 211 (Cherokee Co., SC) due to the occurrence of metals (cadmium, chromium, copper, lead, and zinc) in excess of the aquatic life acute standards. The aquatic community was not fully supported at the Columbia Water Plant diversion canal due to the occurrence of copper and zinc in excess of the aquatic life acute standard. The aquatic community may not be fully supported in the Parr Shoals Tailrace at SC 213 (Richland Co., SC) due to the occurrence of pesticides (P,P'DDT, P,P'DDE, endrin) and PAH's (benzo(k)Fluoranthene, chrysene, fluoranthene, phenathrene, and pyrene). Recreational uses were not supported in the Broad River at SC 18 in Cherokee County due to the presence of fecal coliform bacteria. Recreational uses were partially supported at SC 211 (Cherokee Co., SC), SC 215 (Union Co., SC), SC 34 (Newberry Co., SC), SC 213 (Richland Co., SC), and the Columbia diversion canal, also because of the presence of fecal coliform bacteria.

Sample Sites

Ten areas distributed along the length of the river were selected for sampling (Figure 1) based on three main criteria: access ability; provided a variety of aquatic habitats (riffle, run and pool); and located in the most riverine areas between dams. Area 1, located below Bookman Island (34°13'46.8", 81°13'84.5") is the only sample area below Parr Shoals Reservoir. Two sample areas were chosen between Neal Shoals and Parr Shoals Reservoirs to try to account for the possible influence of poor water quality from the Tyger River on the fish community of the Broad River. Area 2 (34°43'15.1", 81°41'04.7") is located directly below the confluence of the Tyger River 22 km above Parr Shoals Dam. Area 3 (34°55'73.0", 81°42'27.3"), located above the confluence of the Tyger River, is 2 km below the Sandy River Boat access. Area 4 is located 4 km below Lockhart Reservoir (34°75'89.9", 81°45'52.3"). Two sample areas are located in the river reach from Ninety-Nine Islands to Lockhart Reservoir. Area 5 (34°83'72.8", 81°45'80.3") is directly below the Pacolet River and Area 6 (34°99'53.5", 81°48'42.2") is at Smiths Ford. Area 7 (35°05'33.3", 81°53'82.5") is located 2 km below the Cherokee Falls Dam. Two sample areas were selected between the Gaston Shoals and Cherokee Falls hydro-power dams to try to account for the possible influence of poor water quality from Canoe Creek on the fish community of the Broad River . Area 8 (35°09'96.1", 81°57'36.6") is located 5 km above Cherokee Falls Dam and directly below Canoe Creek. Area 9, located above the confluence with Canoe Creek, is 2 km below Gaston Shoals Dam and directly above Buffalo Creek (35°11'79.0", 81°57'63.0"). Area 10 is located 5 km above Gaston Shoals Dam (35°16'84.6", 81°61'84.7"). Additional sampling will likely occur in the bypassed sections of the Broad River at the Gaston Shoals and Lockhart hydro-projects.

Methods

Aquatic Community Sampling

Fish community sampling will be conducted at ten fixed sampling areas during the Spring of 2001 and 2002 (April - May) and the Fall of 2000 and 2001 (October - November). Each sampling area will consist of a 1.6 km reach of river containing navigable pool/run habitat and accessible riffle areas. Fish will be collected by boat electrofishing, backpack electrofishing and seining. Boat electrofishing will be conducted in pool/run habitat and backpack electrofishing and seining will be used in complex habitat areas associated with shoals and islands.

A sample in pool/run habitat will consist of boat electrofishing three randomly selected sites within a sample area. Two sites will be shoreline sections and one site will be a mid-channel section. Each site will receive 10 minutes of electrofishing effort. Electrofishing will proceed in a downstream direction and shocking time will be continuous (i.e., no switching the power on and off will occur). Electrofishing output will be standardized and electrofisher on time will be recorded. All stunned fish will be netted and placed in a live-well. Each fish collected will be identified to species. The total catch and the total weight for each non-game species will be recorded. Total length will be recorded from 25 individuals of each non-game species. Total length and individual weights will be recorded for each game species. Taxonomically difficult specimens will be sent to outside experts for confirmation; a reference collection will be maintained.

To assess fish population structure, total length (mm), total weight (g), and sex will be obtained during the fall from all specimens of black bass Micropterus spp., redbreast sunfish Lepomis auritus, and channel catfish Ictalurus punctatus. Otoliths or spines will be collected to estimate growth of these species. Fish Health Assessment Index (FHAI) scores for largemouth bass will be calculated at each sample area during the Fall, 2001. Fifteen largemouth bass ($250 mm and # 450 mm) will be collected from each sample area; the methods described by Coughlan et al. (1996) will be used to construct FHAI scores.

Backpack electrofishing and seining in complex habitats (i.e., shoals and islands) will be used to augment fish community information obtained from boat electrofishing pool/run habitat. A modification of the Tennessee index of biotic integrity (TIBI) protocol will be used for sampling complex habitat. The sampling protocol is designed to deplete species from dominant habitats (riffles, runs, pools and shorelines). Each of these habitats will be sampled (except shorelines) until three consecutive units of effort produce no additional species for that habitat. Within riffle and run habitat each unit of effort will consist sampling 225 square feet (e.g.,15 ft by 15 ft). A 15 ft seine will be positioned perpendicular to the current; one person outfitted with a backpack electrofishing unit will begin shocking 15 ft above the seine and shock downstream into the seine. If suitable pools are available seine hauling will be used to sample pool habitats. If shallow (< 1.5 m) shoreline areas are available backpack electrofishing will be conducted upstream for 100 m. All fish captured during sampling, except large specimens (>125 mm), will be preserved and taken back to the lab for processing. In the lab preserved fish will be sorted by species, enumerated, weighed, and examined for external anomalies. Total length will be recorded for 25 individuals of each species collected. Taxonomically difficult specimens will be verified by outside experts and a reference collection maintained.

A qualitative mussel and crayfish survey will be conducted at each complex area sampling site. Crayfish collected during fish sampling will be preserved and taken back to the lab for identification. A visual mussel search will be performed at each site. Two people equipped with view buckets will search for 15 min at each site; the species (except Corbiculoidea sp.) of each live mussel encountered will be recorded.

Parameters collected and calculated

Water temperature, dissolved oxygen, conductivity, pH, turbidity, river stage, and habitat variables will be recorded at each sample location before electrofishing. The qualitative habitat survey will include classifying the sample site as pool, run or riffle, determining the primary and secondary substrate components, determining mean depth, and identifying the primary source of cover. Water quality and habitat variables will be used to provide a measure of sampling consistency and to investigate possible biological interactions.

Data obtained from boat and backpack electrofishing will be used to calculate relative abundance, species diversity, and species richness metrics for the fish community at each sample area. Catch per unit effort (CPUE; no./hr) and weight per unit effort (KPUE; kg/hr) will also be determined. Appropriate statistical techniques will be used to investigate differences among sample areas.

Data interpretation and analysis

Objective 1 - The fish collection techniques selected for this study should provide and adequate inventory of the fish fauna of the Broad River. The collection location of each species will be entered into a geographic database and a reference collection of all fish species collected from the Broad River will be assembled. Locations of each mussel and crayfish species encountered will be included in the geographic database.

Objective 2 - A quantitative similarity coefficient, such as the Bray-Curtis measure of similarity will be used to determine if fish communities differ among sites. This technique will be used to investigate longitudinal changes in the fish community, examine the possibility of fish community fragmentation associated with dams and to determine if the fish community differs above and below tributaries with poor water quality (i.e., Canoe Creek and Tyger River).

Objective 3 - An appropriate statistical technique, such as stepwise multiple regression will be used to determine the relationship among dependent variables (i.e., fish species richness, FHAI scores, CPUE), and distance from a dam, dissolved oxygen concentration, pH, turbidity, conductivity, temperature, percent forested land within 1 km of the sample site, and river stage at the time of sampling.

Objective 4 - Fish community and environmental (i.e., landuse, water quality and habitat) data collected during the study will hopefully identify areas which require enhancement or protection.

Geographic Database

A geographic database for the Broad River will be developed using Arc/View software. The database will include several layers of information comprising access areas, historic fish sampling sites, current sampling sites, water quality sampling sites, riparian land cover, USGS gages, and a habitat map. The habitat map will show the locations of riffles, runs, pools, glides, and shoals along the course of the river. The use of a GIS will aid in the identification of perturbations and facilitate spatial analyses of the data.

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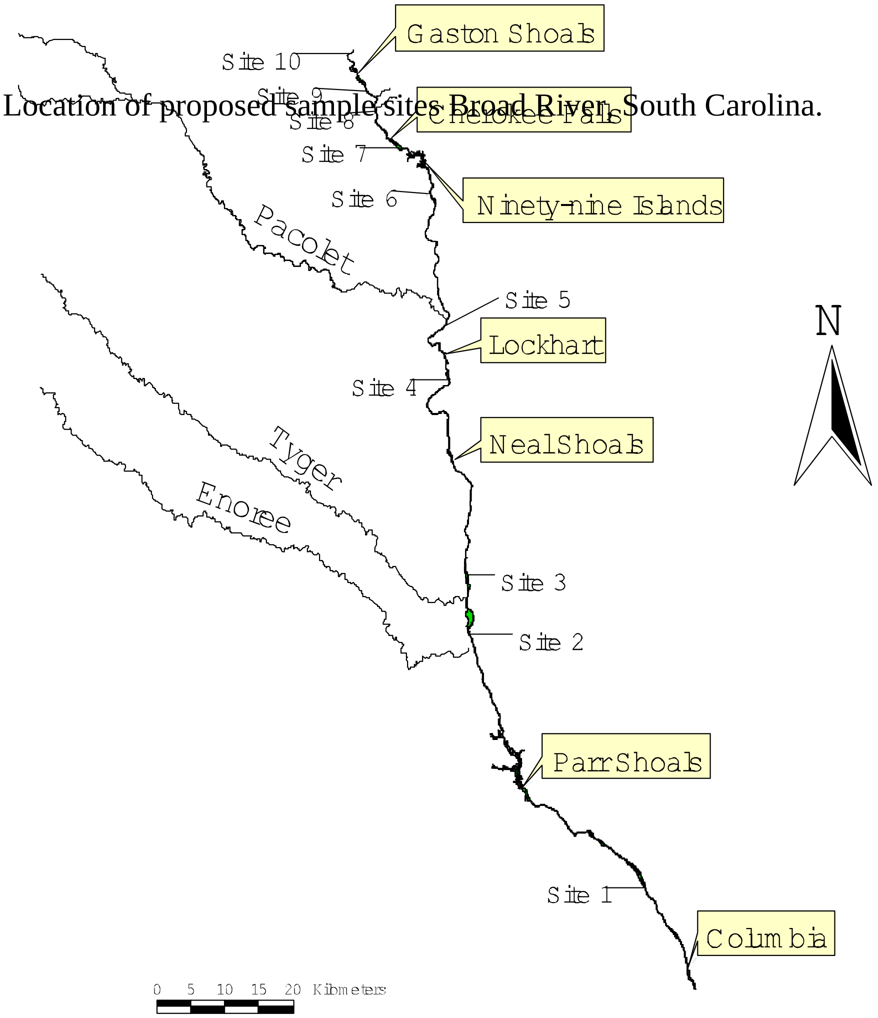


Figure 1. Location of proposed sample sites Broad River, South Carolina.

JOB PROGRESS REPORT

STATE: South Carolina GRANT NUMBER: Sea Grant

PROJECT TITLE: Fisheries Investigations in Lakes and Streams - Statewide

STUDY: Research

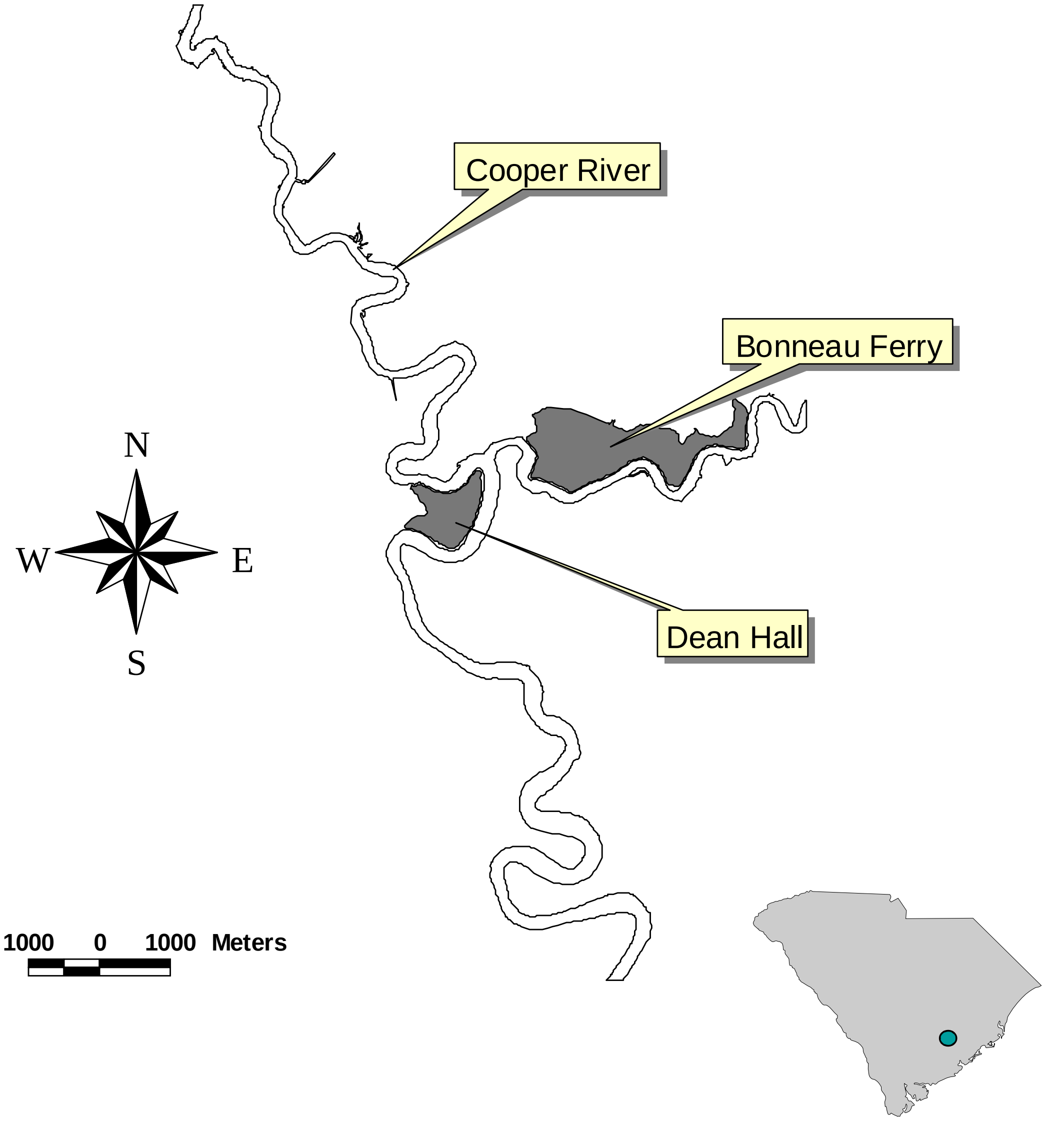
JOB TITLE: Inventory of the fish community of tidal freshwater wetlands of the Cooper River

SEGMENT DATES: 1 July 1999 through 30 June 2000

Introduction

The upper portion of the Cooper River is made up of large expanses of abandoned rice fields which now interact with the river as tidal wetlands (Homer and Williams 1985; Figure 1). The rediversion of flows from the Cooper River to the Santee River reduced the average annual flow from 448 cubic meters per second (cms) to 84 cms and dropped the mean water level by 30%. The rediversion and subsequent reduction in mean water level accelerated the succession of the plant communities in these wetlands (South Carolina Department of Health and Environmental Control, Office of Ocean and Coastal Resource Management 2000). Our objective was to compare the fish communities between two abandoned rice fields, Dean Hall and Bonneau Ferry, in different stages of plant succession.

Figure 1.–Map of Cooper River, South Carolina showing locations of Dean Hall and Bonneau Ferry ricefields where comparisons of fish communities were made.



Methods

Study Site

Dean Hall (DH; Figure 1) is a 63 ha wetland in the later stages of plant succession and is comprised of 73% intertidal, emergent vegetation with such species as pickerel weed *Pontederia cordata*, arum *Peltandra virginica*, and giant cutgrass *Zizaniopsis miliacea* (McManus 2000). The dominance of intertidal, emergent vegetation makes DH navigable by motorboats only through channels even at high tide.

Bonneau Ferry (BF; Figure 1) is a 96 ha wetland in the middle stages of plant succession, comprised of 43% open water vegetation, such as coontail *Ceratophyllum demersum*, fanwort *Cabomba carloliniana*, elodea *Egeria densa*, and hydrilla *Hydrilla verticillata*, and 20% intertidal, emergent vegetation (McManus 2000). Bonneau Ferry is navigable throughout the entire wetland at high tide by most motorboats, through channels at low tide by small motorboats, and throughout the entire wetland at low tide only by shallow water crafts such as a fan boat.

Data Collection

Electrofishing.–We set up fixed stations of 200 m transects in both wetlands and electrofished each transect every other month beginning in April 1999 through February 2000. There were four stations in DH and eight in BF. Four stations in BF were selected in channels, to be similar to the ones in channelized DH, and the other four were selected arbitrarily. Sites were electrofished during the day with a boat mounted electrofishing unit at four different tide stages against the incoming tide. Tide stage 1 was defined as 2 hours above low tide until 3 hours before high tide, stage 2 was 3-2 hours before high tide, stage 3 was 2-1 hours before high tide, and stage 4 was 1 hour before and up to high tide. Fish were captured, identified, measured to the nearest 1-mm, and released. Fish whose identities were uncertain were taken to the lab for identification.

Drop Trap.–We used drop traps (Jordan et al. 1997) to sample smaller fishes inhabiting the wetlands. Each wetland was divided up into three blocks, upriver, middle, and downriver. Blocks were selected at random and 30 drop trap samples were taken from each block. Each wetland was sampled over three consecutive days, every other month, from March 1999 through January 2000. We used a bar seine, the width of which equalled the width of the drop trap, and made passes within the trap until no fish were found through three consecutive passes. Fish were captured and preserved in 10% formalin until identification and measurement could be made in the lab.

Statistical Methods

Using the electrofishing data from April through December 1999, I compared mean catch rates (number of fish per meter of electrofishing) between the two ricefields with ANOVA. I used EstimateS (Colwell 1997) to calculate Horn's index of similarity to compare the similarity of the fish communities between Dean Hall and Bonneau Ferry which ranges from 0 (no species in common) to 1 (all species in common). I then used canonical correspondence analysis (ter Braak 1995) to test for differences in the fish communities between the two ricefields. I supplied the name of the ricefield as the environmental variable. Since there were only two environmental variables, a randomization test of the first axis (a ricefield axis since there were only two) would give the probability that the ordination could occur by chance and is essentially a test of differences of the fish communities between the two ricefields. No statistical tests were performed using drop trap data.

Results

Electrofishing

Based on data from April through December 1999, 26 species were captured in Dean Hall and 27 in Bonneau Ferry (Table1). Significantly more individuals per meter were found in Dean Hall compared to Bonneau Ferry ($\underline{P} < 0.01$; Table 2). Horn's index of similarity of fish communities between ricefields was 0.794. The canonical correspondence analysis showed that the fish communities differed between wetlands ($\underline{P} < 0.01$; Figure 2). Those species to the farthest left of the diagram were those species found only in Dean Hall while those species to the farthest right were those found only in Bonneau Ferry. In the middle were those species found in equal abundance in both ricefields.

Drop Trap

Most results from drop trap data are preliminary and no statistical tests have been performed. From March 1999 through January 2000, we have captured 13,156 individual fish from both wetlands collectively. Bonneau Ferry samples contained 12,077 individuals representing 24 species whereas Dean Hall samples contained only 4,407 individuals representing 24 species (Table 1).

Table 1.–List of species captured by electrofishing and drop traps in Dean Hall (DH) and Bonneau Ferry (BF) wetlands in the Cooper River, South Carolina from April 1999 through January 2000.

		Dean Hall		Bonneau Ferry	
Scientific Name	Common Name (Abbr.)	Electrofishing	Drop Trap	Electrofishing	Drop Trap
Amiidae					
Amia Calva	Bowfin (BFN)	X		X	
Anguillidae					
Anguilla rostrata	American eel (AEL)	X	X	X	X
Aphredoderidae					
Apredoderus sayanus	Pirate perch (PIP)			X	X
Atherinidae					
Labidethses sicculus	Brook silverside (BSS)	X			
Menidia beryllina	Inland silverside (ILS)	X	X	X	X
Belonidae					
Strongylura marina	Atlantic needlefish (ANF)	X			
Bothidae					
Paralichthys lethostigma	Southern flounder (SFL)	X		X	X
Centrarchidae					
Lepomis punctatus	Spotted sunfish (SOS)	X	X	X	X
Lepomis auritus	Redbreast sunfish (RBS)	X	X	X	
Lepomis microlophus	Redear sunfish (RES)	X	X	X	X
Lepomis macrochirus	Bluegill (BLG)	X		X	
Enneacanthus glorisus	Bluespotted sunfish (BLS)	X	X		
Enneacanthus obesus	Banded sunfish (BDS)	X			

Table 1.-Continued

		Dean Hall		Bonneau Ferry	
Scientific Name	Common Name	Electrofishing	Drop Trap	Electrofishing	Drop Trap
Centrarchidae					
Elassoma zonatum	Banded pygmy sunfish (BPS)			X	
Micropterus salmoides	Largemouth bass (LMB)	X	X	X	X
Clupeidae					
Dorosoma cepedianum	Gizzard shad (GZS)			X	
Cyprinidae					
Cyprinus carpio	Common Carp (CRP)			X	
Notemigonus crysoleucas	Golden shiner (GLS)	X	X	X	
Notropis spp.	Shiner (SHINER)				
Eleotridae					
Dormitator maculatus	Fat sleeper (FAS)	X	X	X	X
Eleotris pisonis	Spinycheek sleeper(SCS)		X	X	
Esocidae					
Esox americanus	Redfin pickerel (RFP)	X	X		X
Esox niger	Chain pickerel (CHP)		X	X	X
Fundulidae					
Lucania goodei	Bluefin killifish (BFK)	X	X	X	X
Lucania parva	Rainwater killifish (RWK)	X	X	X	X
Fundulus heteroclitus	Mummichog (MMC)		X		X
Fundulus confluentus	Marsh killifish (MKF)		X		X
Fundulus chrysotus	Golden topminnow (GLT)	X	X	X	X

Table 1.-Continued

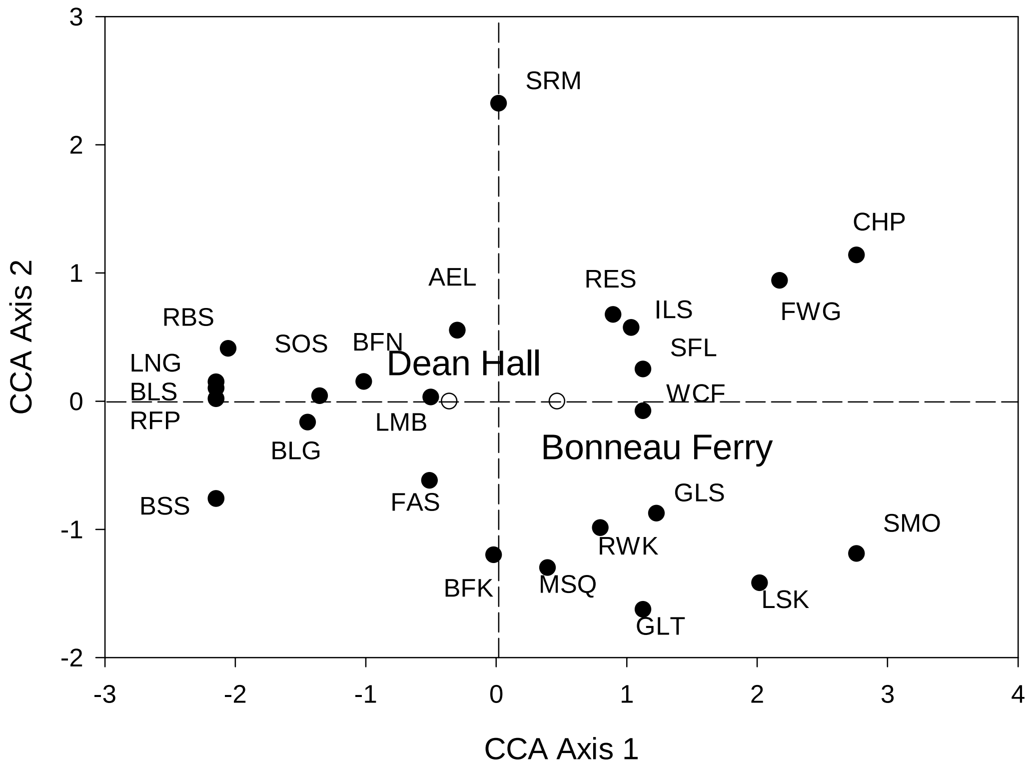
		Dean Hall		Bonneau Ferry	
Scientific Name	Common Name	Electrofishing	Drop Trap	Electrofishing	Drop Trap
Gerreidae					
Eucinostomus argenteus	Spotfin mojarra (SMO)			X	X
Gobbiidae					
Gobionellus shufeldti	Freshwater goby (FWG)	X	X	X	X
Gobionellus shufeldti	Sharptail goby (STG)				
Ictaluridae					
Noturus gyrinus	Tadpole madtom (TPM)		X		X
Ameirus natalis	Yellow bullhead (YBH)	X			
Ameirus catus	White catfish (WCF)	X	X	X	X
Ictalurus furcatus	Blue catfish (BCF)			X	
Lepisosteidae					
Lepisosteus osseus	Longnose gar (LNG)	X			X
Mugilidae					
Mugil cephalus	Striped mullet (SRM)	X		X	
Ophichthidae					
Myrophis punctatus	Speckled worm eel (SWE)		X		
Poeciliidae					
Gambusia holbrooki	Mosquitofish (MSQ)	X	X	X	X
Heterandria formosa	Least killifish (LSK)	X	X	X	X
Poecilia latipinna	Sailfin molly (SFM)				X
Soleidae					
Trinectes maculatus	Hogchoker (HCK)		X		X

Table 2.–Catch rates (mean fish per meter of electrofishing) of fish in Dean Hall and Bonneau Ferry wetlands from April 1999 - December 1999.

Ricefield	Mean	Standard Error
Dean Hall	0.13	0.02
Bonneau Ferry	0.05	0.01

P < 0.01

Figure 2.–Canonical correspondence analysis diagram of fish community data comparing Dean Hall to Bonneau Ferry based on electrofishing in April through December 1999. Open circles denote site scores for wetlands and closed circles denote site scores for species. Species abbreviations are found in Table 1.



Discussion

Differences between the two ricefields were evident, but not to a great extent. Based on electrofishing, Dean Hall contains more sunfish whereas Bonneau Ferry contains more killifish. Moreover, Dean Hall contains more total fish. However, drop trap data suggests the opposite trend in total fish abundance with Bonneau Ferry containing three times the number of fish as Dean Hall. These results suggest that Dean Hall contains larger fish, those more susceptible to electrofishing, than Bonneau Ferry. Additionally, the channelization of Dean Hall affected the estimates of fish abundance since the standard errors around the mean catch rates were twice those for Bonneau Ferry.

Further analyses are needed to determine more subtle differences in the fish communities between these two ricefields. Additionally, more work will be forthcoming relating fish abundance to plant density. South Carolina Sea Grant requires an annual report by April 30, 2001 and a final report by April 30, 2002 which will contain this information.

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